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Sequence 2, Appli
Sequence 1676, A
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APPLICANT: Day, Kun
APPLICANT: Day, Kun
APPLICANT: Clark, Kenneth
APPLICANT: Clark, Kenneth
APPLICANT: Lyashchenko, Yuri
TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REPERENCE: A3278A-US
CURRENT APPLICATION NUMBER: US/09/526,043
CURRENT FILING DATE: 2000-03-14
EARLIER APPLICATION NUMBER: 60/125,108
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
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Sequence 27
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Sequence 27
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100.0%; Pred. No. 8.4e-141;
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US-08-712-709-5

US-09-11-444-5

US-09-541-228-5

US-09-772-647-4

US-09-772-647-4

US-09-538-092-1003

US-09-949-016-7606

US-09-949-016-7606

US-09-949-016-7547

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US-09-538-092-853

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US-09-538-092-943

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US-08-681-219A-27

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US-08-313-274-2
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; Sequence 2. Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
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SEQ ID NO 2
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296; Conservative
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TYPE: PRT
ORGANISM: Hômo sapiens
US-09-526-043-2

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Sequence 1053, Ap
Sequence 139, App
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Sequence 157, Appl
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                   version 5.1.7
- 2006 Biocceleration Ltd.
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2. /GgnZ_6/prodata/1/iaa/6_COMB.pep:*

3. /GgnZ_6/prodata/1/iaa/H_COMB.pep:*

4. /GgnZ_6/prodata/1/iaa/PGTNS_COMB.pep:*

5. /GgnZ_6/prodata/1/iaa/RE_COMB.pep:*

6. /GgnZ_6/prodata/1/iaa/RE_COMB.pep:*

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US-09-771-161A-223
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US-09-771-161A-139
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100.0%; Score 1563; DB 2; Length
Best Local Similarity 100.0%; Pred. No. 8.8e-141;
Matches 296; Conservative 0; Mismatches 0; Indels
                  0; Indels
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Sequence 248, Application US/09771161A
Sequence 248, Application US/09771161A
Setent No. 6936450
GENBEAL INFORMATION:
APPLICANT: LEVINE, et al.,
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION UNMBER: US/09/771,161A
CURRENT APPLICATION NUMBER: 09/724,676
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-16-15
PRIOR FILING DATE: 2000-16-15
PRIOR FILING DATE: 2000-16-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
SPRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
SPRIOR FILING DATE: 2000-06-15
TYPES PRIOR FILING DATE: 2000-06-15
SEQ ID NO 248
LENGTH: 479
TYPE: PRI PRI THE PRI T
                  0; Mismatches
                  296; Conservative
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US-09-771-161A-248
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100.0%; Pred. No. 8.8e-141;
Ative 0; Mismatches 0;
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APPLICANT: LEVINE, et al.,
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES;
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES;
FILE REPRENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2000-10-26
PRIOR PELICATION NUMBER: 09/724,676
PRIOR PELICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE PATENTIAN VARIANTALIAN VARIANTA
                                                                                   GENERAL INFORMATION:

APPLICANT: LEVINE, et al.

ITLE OP INVENTION:

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT APPLICATION NUMBER: 09/724,676

PRIOR FILING DATE: 2000-10-26

PRIOR FILING DATE: 2000-16-15

PRIOR FILING DATE: 2000-06-15

SOFTWARE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0
Sequence 246, Application US/09771161A
Patent No. 6936450
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Patent No. 6936450
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Best Local Similarity 100.
Matches 296; Conservative
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US-09-771-161A-246
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ORGANISM: Homo sapiens
US-09-771-161A-247
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Best Local Similarity
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US-09-771-161A-247
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Sequence 2, Application US/09590740 Patent No. 6689807
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ORGANISM: Homo sapiens
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                                        GENERAL INFORMATION:
APPLICANT: Guo, Kun
APPLICANT: Clark, Kenneth
APPLICANT: Clark, Kenneth
APPLICANT: Usanchenko, Yuri
TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: A3278A-US
CURRENT FALLING DATE: 2000-03-14
EARLIER PILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARK: Patentin Ver: 2.1
SEQ ID NO 17
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; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer 
WS-09-526-043-17
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APPLICANT: Kenneth Walsh
APPLICANT: Kenneth Walsh
APPLICANT: St. Elizabeth's Medical Center
TITLE OF INVENTION: Homocing Angiogenesis
FILE REPERENCE: 49,784 (1417)
CURRENT APPLICATION NUMBER: US/09/590,740
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FREESEQ for Windows Version 3.0
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87.8%; Pred. No. 1.1e-124;
cive 20; Mismatches 15;
           Sequence 17, Application US/09526043 Patent No. 6881555
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Best Local Similarity 87.8
Matches 260; Conservative
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US-09-526-043-17
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US-09-590-740-6
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266 SEKNVVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDND 325
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                                                                                                                                    122 SGK-IVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                                                     181 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
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87.8%; Pred. No. 1.3e-124;
iive 20; Mismatches 15; Indels
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| Sequence 1053, Application US/09538092
| Patent No. 6753114
| GENERAL INFORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Mansfield, Traci A. TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
| CURRENT APPLICATION NUMBER: US/09/538,092
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 1300-02-01
| NUMBER OF SEQ ID NOS: 1387
| SEQ ID NOS: 1387
| SEQ ID NOS: 1387
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llarity 87.8%; Pred. No. 1.3e-124;
Conservative 20; Mismatches 15; Indels 1;
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.7. OTHER PRORMATION: Polypeptide Accession Number P31749
US-09-538-092-1053
          APPLICANT: Kenneth Walsh
APPLICANT: Kenneth Walsh
APPLICANT: St. Elizabeth's Medical Center
TITLE OF INVENTION: HMG COA Reductase Inhibitors for
TITLE OF INVENTION: Promoting Angiogenesis
FILE REFERENCE: 49,784 (1417)
CURRENT APPLICATION NUMBER: US/09/590,740
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 260; Conserv
GENERAL INFORMATION
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206 RHPPLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLH 265
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Sequence No. 688155

GENERAL INFORMATION:

APPLICANT: Glark, Kenneth

APPLICANT: Clark, Kenneth

APPLICANT: Idvashchenko, Yuri

TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF

FILE REFERENCE: A32784-US

CURRENT APPLICATION NUMBER: 60/125,108

EARLIER APPLICATION NUMBER: 60/125,108

EARLIER APPLICATION NUMBER: 60/125,108

MUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1
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87.8%; Pred. No. 1.3e-124;
iive 20; Mismatches 15;
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US-09-771-161A-223
Sequence 223, Application US/09771161A
Patent No. 6936450
GENERAL INFORMATION:
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Matches 260; Conservative
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US-09-526-043-14
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ole THANDER.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An II TITLE OF INVENTION: On A Cellular Response
FILE REPERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.0
SEQ ID NO 139
LENGTH: 727
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APPLICANT: Pagnoni, Marco
APPLICANT: Clark, Kenneth
APPLICANT: Ivashchenko, Yuri
TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
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US-09-417-197-139
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US-09-526-043-13
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APPLICANT: Ole THASTRUD, et al.
APPLICANT: Ole THASTRUD, et al.
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To 1;
TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0110P
CURRENT APPLICATION NUMBER: US/09/417,197
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 71
LENGTH: 726
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89.2%; Score 1393.5; DB 2; Length 726;
Best Local Similarity 87.8%; Pred. No. 2.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                      89.2%; Score 1393.5; DB 2; Length 480; 87.8%; Pred. No. 1.3e-124; Live 20; Mismatches 15; Indels 1;
APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILLE REPERENCE: 802620-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26
PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 273

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 223

LENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 71, Application US/09417197; Patent No. 6518021
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Matches 260; Conservative
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APPLICANT: Giot, Loic
APPLICANT: Manefield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15566-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/12/352
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 1054
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86.4%; Pred. No. 2.38-124;
Live 23; Mismatches 17; Indels
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; OTHER INFORMATION: Polypeptide Accession Number P31751
US-09-538-092-1054
FILE REFERENCE: A3278A-US
CURRENT APPLICATION NUMBER: US/09/526,043
CURRENT FILING DATE: 2000-03-14
CURRENT FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 480
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Patent No. 6753314
GENERAL INFORMATION:
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Best Local Similarity 86.44
Matches 255; Conservative
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NAME/KEY: misc_feature
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 255; Conserv
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Search completed: February 13, 2006, 06:43:19 Job time : 74 secs

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RESULT 2
US-10-394-568-2
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Sequence 246, Appli
Sequence 247, Appli
Sequence 248, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 108, Appli
Sequence 17, Appli
Sequence 10669, A
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10649, A
7, Appli
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                                                           February 13, 2006, 06:59:09; Search time 281 Seconds (without alignments) 440.133 Million cell updates/sec
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1563
1 KTWANDFDYLKLIGKGTFGKV......VPPFKPQVTSETDTRYFDEE 296
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
        GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-394-568-2
US-10-394-568-12
US-10-394-568-12
US-09-771-161A-246
US-09-771-161A-247
US-09-771-161A-248
US-10-394-322A-3
US-10-217-555-33
US-10-217-555-33
US-10-753-267-108
US-10-753-267-108
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US-10-732-923-10650
US-10-732-923-10650
US-10-732-923-10650
US-10-732-923-10650
US-10-732-923-10650
US-09-771-161A-223
US-09-570-000-4
US-09-570-000-14
US-10-394-322A-1
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US-10-217-555-31
US-10-701-490-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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APPLICANT: Guo, Kun
APPLICANT: Guo, Kun
APPLICANT: Cauch, Marco
APPLICANT: Lagranoi, Marco
APPLICANT: Lagranoi, Marco
APPLICANT: Trashchenko, Yuri
TITLE OF INVENTION: ART NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
TITLE OF INVENTION: AA2794-US
CURRENT APPLICATION NUMBER: US/09/526,043
CURRENT FILING DATE: 1999-03-14
EARLIER APPLICATION NUMBER: 60/125,108
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.2
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Sequence
Sequence
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US-10-713-678-2

US-10-746-545-36

US-10-621-485A-1

US-10-621-485A-1

US-10-823-433-4

US-09-955-99-96

US-10-103-256-11

US-10-103-256-11

US-10-072-036-11

US-10-072-036-11

US-10-072-036-12

US-10-746-545-22

US-11-021-951-163

US-11-021-951-163

US-10-146-545-24

US-10-146-545-24

US-10-146-545-24

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US-09-526-043-2
is Sequence 2, Application US/09526043; Publication No. US20030100049A1
igeneral information:
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CRGANISM: Homo sapiens
US-09-526-043-2
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1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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TYPE: PRT
CRGANISM: Homo sapiens
US-11-063-691-2
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; Bedication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: CLARK, KENNETH L.
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; TILLE OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT
; FILE REFERENCE: A3399WO
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR RILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 465
; Sequence 2, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: IVASHCHENKO, YURI
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; TITLE OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT
; TITLE OF INVENTION: US/10/394,568
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; RIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2.
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Best Local Similarity 100.0%;
Matches 296; Conservative C
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; ORGANISM: Homo sapiens
US-10-394-568-12
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US-10-394-568-2
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                                                                                                                          121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
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APPLICANT: Cauch, Kun
APPLICANT: Pagnoni, Marco
APPLICANT: Pagnoni, Marco
APPLICANT: Clark, Kenneth
TITLE OF INVENTION: Arr NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
TITLE REFERENCE: A3278A-US
CURRENT APPLICATION NUMBER: US/11/063,691
CURRENT FILING DATE: 2005-02-23
PRIOR PLING DATE: 2000-03-14
PRIOR PLING DATE: 2000-03-14
PRIOR PLING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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                         143 KTWNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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181 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
                                                                                                                                            61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 120
                                                                                                                                                                    203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 262
                                                                                                                                                                                                                                                               263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 322
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CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 273
SOPTWARE: Patentin version 3.0
SSOTUM 248
LENGTH: 479
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Sequence 248, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
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Matches 296; Conservative
  296; Conservative
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ORGANISM: Homo sapiens
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Fatent No. US20020110811A1
GENERAL INDOMATION:
APPLICATION SET AND SET APPLICATION OF PROTEIN KINASES
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 13676
PRIOR FILING DATE: 2000-01-128
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.0
SEQ ID NO 247
LENGTH: 479
                                                        APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REPERENCE: 802620-2005.1
FURRENT APPLICATION NUMBER: U$/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR PILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-128
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PATCHIN VENEION 3.0
SEQ ID NO 246
LENGTH: 479
Sequence 246, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
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US-09-771-161A-247
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; ORGANISM: Homo sapiens
US-09-771-161A-246
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Best Local Similarity
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US-09-771-161A-247
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Sequence 33, Application US/10217555

Sequence 33, Application WS/10217555

Publication No. US20040009569A1

GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Wind Setting Applicant Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for TITLE OF INVENTION: Kinase Activation
FILE REFERENCE: 44236
CURRENT APPLICATION NUMBER: US/10/217,555
CURRENT APPLICATION NUMBER: GB 0119860.5
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 40
SOFFWARE: Patentin Ver. 2.1
TTYPE: PRIOR TITLE OF THE CALL OF TH
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100.0%; Pred. No. 2.1e-111; tive 0; Mismatches 0;
Best Local Similarity 100.
Matches 296; Conservative
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                        Sequence 3, Application US/10394322A
Publication No. US2003023291A1
GENERAL INFORMATION:
APPLICANT: SUNGESTS PHARMACEUTICALS, INC.
APPLICANT: Prescott, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT FILING DATE: 2003-03-20
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Hommings, Brian A
APPLICANT: Hommings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures
FILE REFERENCE: 44237
CURRENT APPLICATION NUMBER: US/10/217,574
CURRENT APPLICATION NUMBER: US 0119860.5
FRIOR APPLICATION NUMBER: GB 0119860.5
FRIOR FILING DATE: 2001-08-14
FRIOR FILING DATE: 2002-05-01
FRIOR APPLICATION NUMBER: GB 0209985.1
FRIOR APPLICATION NUMBER: GB 0216215.4
FRIOR FILING DATE: 2002-07-12
FRIOR FILING DATE: 2012-07-13
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Publication No. US20040005687A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 296; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 479
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TRHPFLISLKYSFQTKDRLCFVMBYVNGGBLFFHLSRERVFSEDRTRFYGAEIVSALDYL 120
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323 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKPPRTLGSDAKSLLSGLLI 382
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APPLICANT: Guo, Kun
APPLICANT: Pagnoni, Marco
APPLICANT: Pagnoni, Marco
APPLICANT: Pagnoni, Marco
APPLICANT: Ivashchenko, Yuri
TITLE OF INVENITON: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: A3278-U8
CURRENT FILING DATE: 2000-03-14
EARLIER FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 454
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APPLICANT: Pagnoni, Marco
APPLICANT: Pagnoni, Marco
APPLICANT: Clark, Kenneth
APPLICANT: Lyashchenko, Yuri
TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: A3278A-US
CURRENT APPLICATION NUMBER: US/11/063,691
PRICR APPLICATION NUMBER: US/9/526,043
PRICR FILING DATE: 2000-03-14
                                                                                            OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
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                                                                                                                                                                                                                                                                                                                ; Sequence 17, Application US/09526043; Publication No. US20030100049A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT .
ORGANISM: Artificial Sequence
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Matches 295; Conservative
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APPLICANT: Galvin, Katherine M.
APPLICANT: Calvin, Katherine M.
APPLICANT: Donoglue, Mary A.
APPLICANT: Donoglue, Mary A.
APPLICANT: Tomilison, James E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 10653, 2255, 2166, 17794, 2205, 1102, 21061, 17662, 11112 DF INVENTION: 10653, 2355, 2166, 17794, 23652, 21061, 21071, 817, 11112 DF INVENTION: 10653, 9235, 2166, 17794, 23652, 21061, 21071, 817, 11112 DF INVENTION: 3533, 9462, 9123, 12708, 17729, 6552, 1201, 9955, 11112 DF INVENTION: 32345, 9564, 1371, 13319, 41969, 8921, 28695, 554, 16408, 11112 DF INVENTION: 32345, 9564, 1371, 13319, 41969, 8921, 8931, 955, 11112 DF INVENTION: 32345, 9564, 1371, 13319, 41969, 8921, 8931, 955, 11112 DF INVENTION: 40202, 112091, 13864, 13942, 1673, 54946 OR 2419
TITLE OF INVENTION: 40202, 112091, 13864, 13942, 1673, 54946 OR 2419
FILING DATE: 2003-01-13
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-01-18
PRIOR PILING DATE: 2003-02-05
PRIOR PILING DATE: 2003-02-05
PRIOR FILING DATE: 2003-03-25
PRIOR PILING DATE: 2003-03-25
PRIOR FILING DATE: 2003-03-25
PRIOR FILING DATE: 2003-03-25
PRIOR FILING DATE: 2003-03-25
PRIOR PILING DATE: 2003-03-
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                                                                                                                                                                                                                   APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Stagliano, Nancy E.
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                                                                                                                          Sequence 108, Application US/10753267
Publication No. US20050037946A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                        APPLICANT: Stagliano, Nancy E. APPLICANT: Healy, Aileen APPLICANT: Acton, Susan L.
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Best Local Similarity 100.
Matches 296; Conservative
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US-10-753-267-108
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US-10-713-678-6
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Publication No US20030044946A1

Publication No US20030044946A1

GENERAL INFORMATION:

APPLICANT: LONGO, VALTER D.

TITLE OF INVENTION: GENES, MUTATIONS, AND DRUGS THAT INCREASE CELLULAR

TITLE OF INVENTION: RESISTANCE TO DAMAGE AND EXTEND LONGEVITY IN ORGANISMS

TITLE OF INVENTION: RESISTANCE TO HUMANS

FILE REPRENCE: 13764-7068

CURRENT APPLICATION NUMBER: US/10/116,722A

CURRENT FILING DATE: 2002-10-11

PRIOR FILING DATE: 2001-04-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 5

LENGTH: 320
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                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
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87.8%; Pred. No. 1.1e-98;
ive 20; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                             Query Match 99.7%; Score 1558; DB 6; Length 454; Best Local Similarity 99.7%; Pred. No. 4.9e-111; Matches 295; Conservative 0; Mismatches 1; Indels
PRIOR APPLICATION NUMBER: 60/125,108
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 17
LENGTH: 454
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Murine sp.
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129 SEKNVVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDND 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                   2 TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
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                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10713678
Publication No. US20040122077A1
GENERAL INFORMATION:
APPLICANT: Kenneth Walsh
TITLE OF INVENTION: HOG COA Reductase Inhibitors for INTILE OF INVENTION: Promoting Angiogenesis
FILE REFERENCE: 49,784 (1417)
CURRENT APPLICATION NUMBER: US/10/713,678
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/09/590,740
PRIOR FILING DATE: 2000-06-08
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 480
TYPE: PRT
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us-10-601-311-1\_copy\_143\_438.rapbn

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Koji Hayashi
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CORGANISM: Homo sapiens
US-11-109-156-18
US-11-109-156-18
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   Sequence 1158, Applequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 11, Appl Sequence 11,
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                                                                                                                                                                                                            February 13, 2006, 07:01:34; Search time 16 Seconds (without alignments) 242.767 Million cell updates/sec
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Sequence 72,
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/cgn2_6/ptodata/2/pubpaa/1866 NEW PUB. pep:*
/cgn2_6/ptodata/2/pubpaa/1806 NEW PUB. pep:*
/cgn2_6/ptodata/2/pubpaa/1807 NEW PUB. pep:*
/cgn2_6/ptodata/2/pubpaa/1809 NEW PUB. pep:*
/cgn2_6/ptodata/2/pubpaa/1810 NEW PUB. pep:*
/cgn2_6/ptodata/2/pubpaa/1811 NEW PUB. pep:*
/cgn2_6/ptodata/2/pubpaa/1811 NEW PUB. pep:*
                             GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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US-10-821-234-1158
US-10-770-726-28
US-10-329-258-16
US-10-329-558-16
US-10-995-561-855
US-10-995-561-855
US-10-995-561-855
US-11-099-958-1
US-10-095-561-855
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US-11-132-142-1
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US-11-132-142-6
US-10-877-346-72
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length
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Maximum DB
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45, Appl
20, Appl
47, Appl
12, Appl
112, Appl
146, Appl
147, App
147, Appl
14, Appl
11, Appl
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APPLICANT: MINITORIO CONTROL
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APPLICANT: MINITORO CONTROL
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APPLICANT: MA WAKAMATSU
APPLICANT: AM WAKAMATSU
APPLICANT: Relichin Nagai
APPLICANT: Relichin Nagai
APPLICANT: Relichin Nagai
APPLICANT: Chiaki Senoo
APPLICANT: WINDER: US/10/060.065
FILE REPRENCE: 0560-099002
CURRENT APPLICATION NUMBER: US/10/060.065
FRIOR PRILING DATE: 2002-01-29
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-01-1876
PRIOR FILING DATE: 2000-01-11
PRIOR PLILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 18
LENGTH: ABO
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Sequence
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US-11-113-424-183
US-11-113-424-49
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US-11-113-837-20
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US-11-113-837-18
US-11-113-424-46
US-10-113-424-46
US-10-113-424-12
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US-11-113-837-4
US-10-055-877-146
US-10-113-837-19
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US-10-113-837-19
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US-10-055-877-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/11109156
Publication No. US20050250144A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
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Sequence 76, Application US/1077026

Publication No. US20050266409A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AMI01079 (031895-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: US/10/770,726
UNDMBER OF SEQ ID NOS: 48640
                                                                                                                                               APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Vandeghinste, Nick
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter H. M.
TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
FILE REFERENCE: P27,880-A USA
CURRENT APPLICATION NUMBER: US/11/152,366
CURRENT FILING DATE: 2005-06-14
PRIOR APPLICATION NUMBER: 60/579,307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 DPNKRLG-----GGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 SGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 -HPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH
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48.7%; Score 761; DB 6;
Best Local Similarity 48.0%; Pred. No. 2.7e-58;
Matches 143; Conservative 59; Mismatches 92;
                                                          ; Sequence 28, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.3
SEQ ID NO 28
LENGTH: 737
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SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 150; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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US-10-770-726-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1706
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1158
LENGTH: 343
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                                                                                                                                                         SGK-IVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                                                                                                                                                                                                                                                               266 SEKNVVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDND 325
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                                                                                                                         2 TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
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   DB 7; Length 480;
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                                                              Indels
                             ; Pred. No. 1.7e-113; 20; Mismatches 15;
89.2%; Score 1393.5;
87.8%; Pred. No. 1.7e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
                                                              Conservative
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US-10-821-234-1158
                      Best Local Similarity
Matches 260; Conserv
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   Query Match
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US-10-995-561-856

Sequence 856, Application US/10995561

Sequence 856, Application US/10995561

Sequence 856, Application Occupance 856, Application 856, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 EHPFLTHMFCTFQTKENLFFVMEYLNGGDLMYHIQSCHKFDLSRATFYAAEIILGLQFLH 135
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                                                                                                                                                                                                                                                     APPLICANT: Fitz, Lori
APPLICANT: Greco, Rita
APPLICANT: Graudhary Divya
APPLICANT: Graudhary Divya
APPLICANT: Somers, William Stuart
APPLICANT: MOBYAk, Lidia
TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
FILE REFERENCE: 16163-018001
CURRENT APPLICATION NUMBER: US/11/099,958
CURRENT FILING DATE: 2005-04-06
PRIOR FILING DATE: 2004-04-06
PRIOR FILING DATE: 2004-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7;
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48.5%; Pred. No. 1.3e-58;
iive 54; Mismatches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                              Xu, Zhang Bao
Olland, Stephane
Wolfrom, Scott
Malakian, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 48.5
Matches 143; Conservative
                                                                                                                                                                Lin, Laura
Stahl, Mark
Lee, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo
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LENGTH: 705
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Publication No. US20060024233A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GONZALEZ-ZULUETA, MIRELIA
APPLICANT: AGYT-O080US
CURRENT PILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: 60/343,422
FRIOR APPLICATION NUMBER: 60/343,422
FRIOR PILING DATE: 2001-12-27
NUMBER OF SEQ 1D NOS: 29
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                       671 TSAGHPFLVNLFGCFQTPEHVCFVMEYSAGGDLMLHIHSD-VFSEPRALFYSACVVLGLQ 729
                                                                                                                                                                                                                                                               YLHSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLED 178
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                                                                                                                                     KNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALD
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 942
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; Sequence 81, Application US/10770726; Publication No. US20050266409A1; GENERAL INFORMATION: APPLICANT: Wyeth
                 Xu, Zhang Bao
Olland, Stephane
Wolfrom, Scott
Malakian, Karl
Lin, Laura
Stahl, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-10-770-726-81
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ORGANISM: Homo sapiens
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                   3 MNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT-
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                   Indels
48.5%; Pred. No. 3.1e-58; tive 54; Mismatches 93;
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Publication No. US20060003431A1
 Best Local Similarity 48.5%
Matches 143; Conservative
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CORGANISM: Homo sapiens
US-10-995-561-855
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Best Local Similarity
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Matches 143;
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LENGTH: 706
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APPLICANT: Brown, Eugene
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
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APPLICANT: Wolfrom, Society
APPLICANT: Malakian, Karl
APPLICANT: Lin, Laura
APPLICANT: Lin, Laura
APPLICANT: Lee, Julie
APPLICANT: Fitz, Lori
APPLICANT: Greco, Rita
APPLICANT: Somers, William Stuart
APPLICANT: Wooyak, Lidia
TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
FILE REFERENCE: 16163-01801
FILE REFERENCE: 16163-01801
FILE REFERENCE: 16163-01801
FILING DATE: 2005-04-06
FRIOR PILING DATE: 2004-04-07
NUMBER OF SEQ ID NOS: 4
SOFFWARE: FREUSEQ FOR WINDOWS Version 4.0
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Best Local Similarity 48.5%; Pred. No. 3.1e-58;
Matches 143; Conservative 54; Mismatches 93
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APPLICANT: Montigen Pharmaceuticals, Inc.
APPLICANT: Montigen Pharmaceuticals, Inc.
APPLICANT: Montigen Pharmaceuticals, Inc.
APPLICANT: Montigen Pharmaceuticals, Inc.
APPLICANT: Han, Haiyong
APPLICANT: Han, Haiyong
APPLICANT: Basuss, David J.
APPLICANT: Basuss, David J.
APPLICANT: Bashyam, Sridevi
APPLICANT: Marner, Steven L.
APPLICANT: Marner, Steven L.
APPLICANT: On Hoff, Daniel D.
APPLICANT: Or Hoff, Daniel D.
APPLICANT: Or Hoff, Daniel D.
APPLICANT: Or Hoff, Daniel D.
APPLICANT: WANDER: 192014-00003000073
CURRENT APPLICATION NUMBER: US/11/092,168
                                                                     APPLICANT: THE BUTNHAM INSTITUTE
APPLICANT: Sikora, Sergey
APPLICANT: Sikora, Sergey
APPLICANT: Sikora, Sergey
APPLICANT: Godzik, Adam
TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
FILE REFERENCE: 8014-011-US
CURRENT APPLICATION NUMBER: US/11/132,142
PRIOR APPLICATION NUMBER: 60/571,698
PRIOR PAPPLIAND DATE: 2004-05-17
NUMBER OF SEQ ID NOS: 21
SOFTWARER: Patentin version 3.3
SEQ ID NO 13
LENGTH: 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH 121
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US 60/608,529
US 60/511,486
US 60/511,489
PRIOR FILING DATE: 2004-10-14
     Sequence 13, Application US/11132142
Publication No. US20050276818A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/11092168
Publication No. US20050277658A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Xenopus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 132;
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                                                                                                                                  61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 120
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                                                                                                                                                                                                                                                                                                                                         FDYLKLLGKGTFGKVILVREKAS---GKYYAMKILKKEVII--AKDEVAHTLTESRVLKN
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46.1%; Score 720; DB 6; Length 740;
Best Local Similarity 46.5%; Pred. No. 7.1e-55;
Matches 138; Conservative 60; Mismatches 93; Indels
     Length 495;
                                                     93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 129, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche Inc.
TITLE OF INVENTION: HV regulated protein expression FILE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
47.0%; Score 735; DB 6;
48.0%; Pred. No. 2.1e-56;
ative 54; Mismatches 93.
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; DATABASE ACCESSION NUMBER: sw hum/k6a3_human
; DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129
                          Best Local Similarity 48.08
Matches 141; Conservative
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US-11-132-142-13
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LENGTH: 740
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RESULT 15
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                                                                                                                                                                                        Gaps
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                                                                                                                                                                                      7;
                                                                                                                                                     Length 343;
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                                                                                                                                                  Query Match 43.5%; Score 680.5; DB 7; Best Local Similarity 44.4%; Pred. No. 7.1e-52; Matches 131; Conservative 53; Mismatches 104;
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TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
FILE REPERBENCE: 920214,0000300NT3
CURRENT APPLICATION NUMBER: US/11/092,168
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US 10/965,313
US 60/508,529
US 60/511,486
US 60/511,486
PRIOR FILING DATE: 2004-10-14
2003-10-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 343
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bearss, David J.
Vankayalapati, Hariprasad
Bashyam, Sridevi
Munoz, Ruben M.
Warner, Steven L.
Della Croce, Kimiko
Von Hoff, Daniel D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Arizona Board of Regents or
APPLICANT: Montigen Pharmaceuticals,
APPLICANT: Hurley, Laurence H.
APPLICANT: Mahadévan, Daruka
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Publication No. US20050277658A1
GENERAL INFORMATION:
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CRGANISM: Mus musculus
US-11-092-168-4
                                                                                                 ORGANISM: Bos taurus
US-11-092-168-3
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Sequence 14, Application US/11132142
; Sequence 14, Application US/20050276818A1
; Belblication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burninam Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: 06/571,698
; PRIOR PELING DATE: 2004-05-17
; PRIOR PELING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PALENTIN VERSION 3.3
; SEQ ID NO 14
LENTH: 351
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                                                                                                                                                                                                                                                                                       63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLHS 122
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                                                                         Gaps
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44.1%; Pred. No. 2e-51;
ive 54; Mismatches 104; Indels 7.
       Length 341;
                                                                         Indels
43.5%; Score 679.5; DB 7;
44.4%; Pred. No. 8.7e-52;
ive 53; Mismatches 104;
   Query Match
Best Local Similarity 44.44
Matches 131, Conservative
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Matches 130; Conservative
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ORGANISM: Homo sapiens
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Search completed: February 13, 2006, 07:06:26 Job time : 17 secs

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February 13, 2006, 06:28:06; Search time 309 Seconds (without alignments) 420.894 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ing Orima 110014ed	0	Human	Human	Adg85255 Human Chr	Adg85245 Human Chr	Aab19284 Amino aci	Aab13393 Human Akt	Aau79420 Human pro	Human	Abr57474 Human PKB	Adf45034 Human kin	Adn71940 Human ser	Adq88266 Human 141	Aag78021 Akt3 rela		Aab99833 AGC prote	Adj38881 PKBgamma		m	Aay92223 Wild type	Mouse	2 Mouse	Adl25357 ARKS rela
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The present sequence represents a human Akt3 protein. Expression of Akt3 prevents apoptotic cell death induced by apoptotic stimulating kinase 1 (ASK1). The Akt3 polypoptide is useful for inhibiting cell death, preferably in a cardiac mycotye, resulting from hypoxia, apoptosis or necrosis in a patient suffering from mycoardial infarction or ischemia reperfusion injury. The polypeptide is also useful for treating mycoardial infarction or ischemia reperfusion injury. The more appropriated is also useful for treating reperfusion injury is mycoardial ischemia reperfusion injury or is associated with stroke, liver damage, renal failure, organ

Claim 16; Page 64-65; 73pp; English.

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## ALIGNMENTS

Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell death induced by apoptosis stimulating kinase 1 useful for treating myocardial infarction or ischemia reperfusion injury. Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1; hypoxia; apoptosis; necrosis; myocardial infarction; ischemia; reperfusion injury; myocardial ischemia reperfusion injury; stroke; liver damage; renal failure; organ transplantation; coronary artery. Amino acid sequence of a human Akt3 polypeptide. Clark KL, Ivashchenko YD; AAB19011 standard; protein; 465 AA. (AVET ) AVENTIS PHARM PROD INC. 14-MAR-2000; 2000WO-US006574. 99US-0125108P. (first entry) WPI; 2000-638260/61. Pagnoni MF, N-PSDB; AAA96637 WO200056866-A2. Homo sapiens. 19-MAR-1999; 08-FEB-2001 28-SEP-2000. AAB19011; Guo K, RESULT 1 

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11-JUN-1999;
03-NOV-1999;
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                                                                                                                               Gaps
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                                                                                 Length 465;
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transplantation or coronary artery by pass grafting
                                                                                 100.0%; Score 1563; DB 3;
100.0%; Pred. No. 1.1e-155;
ive 0; Mismatches 0;
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Matches 296; Conservative
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with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570 base pairs defined in the specification. Akt3 has carebroprotective, notropic, neuroprotective, antiarthritic, osteopathic, vasotropic and hepatotropic activity, as an inhibitor of apoptosis and/or apoptosis and the specification. Akt3 has carebroprotective, negatotropic activity, as an inhibitor of apoptosis and/or apoptosis of trimulating kinase 1 (ASK1)-induced cell death Akt3 operably linked to a regulatory region is useful for inhibiting cell death in cardiac myocytes resulting from hypoxia, apoptosis or necrosis and for treating myocardial infarction or ischaemia reperfusion injury, particularly that associated with stroke, liver damage, renal failure, organ transplantation or coronary artery bypass grafting. Agonist of Akt3 are useful for improving Akt3 activity during treatment of patients suffering from myocardial infarction or ischeemia reperfusion injury and inhibitors of Akt3 activity dering treatment of patients suffering from myocardial infarction function, improved quality of life and reduced mortality. In patients with existing heart failure, gene therapy with Akt3 retards the concept the activity described in dilation and slows down disease progression.

Section of function inproved quality of life and reduced mortality. In parcess of ventricular dilation and slows down disease progression or death by apoptosis, including Alzheimer's disease tates, involving cell death by apoptosis, including Alzheimer's disease, liver degeneration or
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the encoding polynucleotide hybridises under stringent conditions
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1es 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 465 AA;
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a serine/threonine protein kinase capable of inducing vascular and serine/threonine protein kinase capable of inducing vascular and serine/threonine protein kinase capable of inducing vascular and capable of the sequence was deduced from cDNA (see AAA89264) isolated from a heart cDNA library. Akt3 is shorter than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of the molecules. A claimed method of inducing expression of VeGF in a cell involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding or myocardial ischaemia, or ischaemic, idopathic or hypertrophic or myocardial ischaemia, or ischaemic, idopathic or hypertrophic cardiomyopathy. The result is beneficial collateral blood vessel formation. A claimed method of inhibiting angiogenesis in a patient suffering from a tumour, comprises inhibiting the level of Akt activity comprises introducing an Akt antisense nucleic acid, an intracellular comprises introducing a makt antisense nucleic acid, an intracellular chinding protein (e.g. a scPv) that sepecifically binds the Akt protein, or a nucleic acid encoding a dominant negative form of an Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGRAVDWWGLGVVWYEMMCGRLPPYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                               present sequence is that of human Akt3, a novel Akt isoform. Akt3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akt2; human; protein kinase; vascular endothelial growth factor; VBGF; inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 KTWNDFDYLKLIGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                                                                                                                           Inducing expression of vascular endothelial growth factor, useful for
                                                                                                                                                                                           treating an ischemic condition, e.g. cerebrovascular ischemia, renal ischemia or pulmonary ischemia, comprises administering a serine/threonine protein kinase Akt protein.
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100.0%; Pred. No. 1.1e-155;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                   Example 1; Page 58-59; 67pp; English.
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                                                               Clark K;
                    (AVET ) AVENTIS PHARM PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2001 (first entry)
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                                                             Ivashchenko Y,
                                                                                                        2001-025336/03.
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                                                                                                                             N-PSDB; AAA89264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 465 AA;
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                                                             Guo K,
                                                                                                                                                                                                                                                                                                                                 The
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ZZXBXBXAX
ZXXBXBX
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The present sequence is that of human Akt2, a serine/threonine protein kinase capable of inducing vasular endothelial growth factor (VEGF) expression. A claimed method of inducing expression of VEGF in a cell involves administering Akt2, Akt1 (see AAB19997) or Akt3 (see AAB1996), or a nucleic acid encoding such a protein. The cell is preferably from a patient suffering from an ischaemic condition, especially from a cerebrovascular, renal, pulmonary, limb or myocardial ischaemia, or beneficial collateral blood vessel formation. A claimed method of inhibiting angiogenesis in a patient suffering from a tumour, comprises inhibiting the level of Akt activity in the patient, thereby inhibiting production of VEGF. The method comprises introducing an Akt antisense nucleic acid, an intracellular binding protein (e.g. a scFv) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 TRHPFLISLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                                                                                                                                                  Inducing expression of vascular endothelial growth factor, useful for treating an ischemia, condition, e.g. cerebrovascular ischemia, renal ischemia or pulmonary ischemia, comprises administering a serine/threonine protein thinse Akt protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGRAVDWWGLGVVMYEMMCGRLPFYNODHEKLPELILMEDIKFPRTLSSDAKSLLSGLLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 KDPNKRLGGGPDDAKEIMRHSFFSGVNWODVYDKKLVPPFKPOVTSETDTRYFDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE
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100.0%; Pred. No. 1.1e-155;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 63-64; 67pp; English.
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                                                                                                                                                                                                                                                              Clark K;
                                                                                                                                                                                                                         (AVET ) AVENTIS PHARM PROD INC
                                                                                                                                                                                   99GB-00026058.
                                                                                                                             01-JUN-2000; 2000WO-US015098
                                                                                                                                                                   99US-0138724P
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Best Local Similarity 100.
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               negative form of an Akt
                                                                                                                                                                                                                                                              Ivashchenko Y,
                                                                                                                                                                                                                                                                                                 WPI; 2001-025336/03.
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                                                      WO200077190-A2
                                                                                                                                                                   11-JUN-1999;
                                                                                                                                                                                     03-NOV-1999;
                                                                                          21-DEC-2000
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                                                                                                                                                                                                                                                            Guo K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
ADG85255
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ADG85255;

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The invention relates to a mutant Chrysosporium strain comprising a nucleic acid sequence encoding a polypeptide of interest. A mutant Chrysosporium strain is useful for producing a polypeptide of interest by culturing a mutant Chrysosporium strain under conditions permitting expression of the protein or polypeptide, and recovering the subsequently produced polypeptide of interest. The conditions further permit secretion of the protein or polypeptide of interest. The polypeptides are useful for hydrolysing beta-glucosidic bonds. A polypeptide is useful for hydrolysing beta-xylosidic bonds. The present sequence represents a human Chrysosporium associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN 202
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                     383 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYPDEE 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel mutant Chrysosporium strain comprising nucleic acid sequence encoding polypeptide of interest such as proteases and lipases, the nucleic acid sequence being operably linked to expression-regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parriche M;
241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE
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Zeijl CMJ;
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0
                                                                                                                                                                                                                                                                       beta-glucosidic bond; beta-xylosidic bond; human.
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                                                                                                                                                                                                                                       Human Chrysosporium associated protein #1.
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, Punt PJ, Van
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                                                                                                                            ADG85245 standard; protein; 465
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06-OCT-1999; 99WO-NL000618.
13-APR-2000; 2000US-00548938.
                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2003; 2003US-00394568
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Pynnonen CM,
                                                                                                                                                                                                   (first entry)
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BURLINGAME R P.
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06-OCT-1999;
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                                                                                                                                                              ADG85245;
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(PARR/)
(BOUS/)
(PYNN/)
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                                                                                  RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a mutant Chrysosporium strain comprising a nucleic acid sequence encoding a polypeptide of interest. A mutant Chrysosporium strain is useful for producing a polypeptide of interest by culturing a mutant Chrysosporium strain under conditions permitting expression of the protein or polypeptide, and recovering the subsequently produced polypeptide of interest. The conditions further permit secretion of the protein or polypeptide of interest. The polypeptides are useful for hydrolysing beta-glucosidic bonds. A polypeptide is useful for hydrolysing beta-xylosidic bonds. The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel mutant Chrysosporium strain comprising nucleic acid sequence encoding polypeptide of interest such as proteases and lipases, the nucleic acid sequence being operably linked to expression-regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1563; DB 8; Length 465; 100.0%; Pred. No. 1.1e-155; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olson PT, Sinitsyn AP,
nt PJ, Van Zeijl CMJ;
                                                                    beta-glucosidic bond; beta-xylosidic bond; human.
                                  Human Chrysosporium associated protein #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Punt PJ,
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                                                                                                                                                                                                                                                      98WO-EP006496.
99WO-NL000618.
2000US-00548938.
                                                                                                                                                                                                                      21-MAR-2003; 2003US-00394568
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(first entry)
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nes 296; Conservative
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VAN ZEIJL C M J.
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BURLINGAME R P.
                                                                                                                                                                                                                                                                                                                                                               OLSON P T.
SINITSYN A P.
PARRICHE M.
BOUSSON J C.
PYNNONEN C M.
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                                                                                                                                             US2004002136-A1.
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                                                                                                                                                                                                                                                        06-OCT-1998;
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13-APR-2000;
                                                                                                           Homo sapiens
25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
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Length 479;

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The present sequence represents a human protein kinase B gamma (PKB) polypeptide. PKB is activated by insulin or insulin growth factor 1. Lipid products of phosphoinostiide 3-kinase act in insulin signalling by binding to pleckstrin homology domains of PKB. PKB polynucleotides may be used as a source of probes and primers. PKB polypeptides are used to raise antibodies, which are used in diagnostic assays. The polypeptides are also useful for screening for compounds which affect insulin
                                                                                    322
                                                                                                                 240
                                                                                                                                            382
               TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 262
                                                        HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                       HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
                                                                                                                                YGRAVDWWGLGVVWYZEMYCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
                                                                                                                                                                                                                                                                                                                                                                                               Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1; phosphoinositide 3-kinase; insulin signalling; pleckstrin homology domain.
TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                      KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein kinase B gamma polynucleotides and polypeptides useful as probe or primers in polymerase chain reaction and to raise antibodies useful in diagnostic assays for detecting polypeptide
                                                                                                                                                                                                                                                                                                                                                                   acid sequence of a human kinase B-gamma polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "putative phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "active phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                              AAB19284 standard; protein; 479 AA
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signalling pathways

Sequence 479 AA;

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The present sequence is human Akt-3. Akt-3 is a third human isoform of Akt, which is also known as protein kinase B (PKB) or "related to A and C protein kinase" (RAC-PK). It is located on human chromosome 1, region q43-q44. A human hippocampal EST sequence that showed high similarity to the rat RAC-PKgamma sequence was used to design primers for 3' rapid amplification of cDNA ends (3' RACE). The sequence obtained in the first round of 3' RACE was used to design primers for a second round. The complete sequence was then amplified from human hippocampal cDNA by PCR using primers based on the product of the second round of 3' RACE. Akt can inhibit apoptosis induced by detachment from the extracellular
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                                                                                                                                                                                        HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
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apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
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                                                                                  TRHPFLTSLKYSFQTKDRLCFVMBYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                             203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                          HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human serine/threonine kinase protein and the polynucleotide encoc
the protein, useful for preparing a medicament for treating disorders
associated with human serine/threonine kinase protein activity,
                                                                                                                                                                                                                                                                       323 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKPPRTLSSDAKSLLSGLLI
                                                            1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
                                                                                                                                                                                                                                                       YGRAVDWWGLGVVMYEMWCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
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                                Indels
100.0%; Score 1563; DB 3;
100.0%; Pred. No. 1.2e-155;
iive 0; Mismatches 0;
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N-PSDB; AAA62450, AAA62451.
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                                  Conservative
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                al Similarity
296; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB; gamma secretase; apoptosis; Alzheimer's disease; PS-1; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying an agent modulating interaction between integrin-linked kinase (ILK) and presenting. (FB1) comprisaing providing ILK, PS1 or their functional variants, as first and second components respectively, contacting the components in the presence of a
matrix. The Akt-3 nucleic acid molecule and protein may be used as medicaments for treating cancer. Agents which influence the activity of Akt-3 protein, and so stimulate apoptosis, may also be used to treat
                                                                                                                                                                                                   TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                                     TRHPFLTSLXYSFQTXDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                                                                                            263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                                             1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying agent that modulates interaction between integrin-linked kinase and presenilin-1, useful for treating Alzheimer's disease, and identifying agent that modulates protein kinase B or gamma secretase
                                                                                                                                                                                                                                                                                                                                                             KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
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                                                                                            100.0%; Score 1563; DB 3; Length 479; 100.0%; Pred. No. 1.2e-155;
                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; cytostatic; cancer.
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                                       diseases associated with Akt-3
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                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-351896/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hiles ID, Ellis C;
                                                                                                        Local Similarity
les 296; Conserv
                                                                  Sequence 479 AA;
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                                                                   the method above where the components are protein kinase beta (FKB), and an enthod above where the components are protein kinase beta (FKB), the methods and an agent identified by the methods. The methods are used for identifying an agent that medulates interaction between ILK and FB1. Or FKB or gamma-secretase. The agent has therapeutic applications in treating humans or animals, for treating a host suffering from a condition associated with an interaction between ILK and FB1, activity of gamma-secretase, apoptosis, cancer and Alzheimer's disease. The agent is also useful for manufacturing a medicament for use in treatment of the above mentioned conditions. The present sequence represents human protein kinase B gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEDND 180
test agent under conditions that in absence of the agent, would permit the components to interact and determining whether the agent is capable of modulating the interaction between the components. Also included are
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100.0%; Pred. No. 1.2e-155;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 479 AA;
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The present invention describes the regulation of apoptosis, in which the intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a char-shock protein) is promoted or inhibited. The present invention also describes: (1) isoforms of Akt and Hsp90, and their partial peptides including the binding domain; (2) antibodies to Akt or Hsp90, (3) DNA concluding the binding domain; (4) expression vectors containing the DNA; (5) host cells commain; (4) expression vectors containing the DNA; (5) host cells containing the DNA; (6) production of Akt or Hsp90 or their partial peptides including the binding domain by culture of the cransformed cells; (7) screening compounds for their ability to modify intracellular Akt activity by contact with cells expressing Akt or Hsp90; and (8) drug compositions containing antibodies recognizing the binding domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and Hsp90 have cytostatic, cardiant, vasotropic, hepatotropic, antidiabetic, neuroprotective and nootropic activities. Blockade of the binding of Hsp90 with Akt increases the sensitivity of cells to apoptosis induction. Akt and Hsp90 can be used in the prevention and treatment of diseases with which apoptosis regulation is associated, including cancer (such as gastric cancer, ovarian cancer, breast cancer, pancreatic cancer, ovarian cancer, breast cancer, paresent sequence represents human Akts which is used in the prevention and treatment is schaemia. The prevent is sequenced by the containing the binding concer and concerned to be applied to the prevention and treatment cancer and concerned to be appresent sequence represents human Akts which is used in the
                                                                                         Regulation of apoptosis by promoting or inhibiting the intracellular binding of Akt with Hsp90, useful for prevention and treatment of apoptosis-regulation associated diseases including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention
                                                                                                                                                                                                                      Claim 12; Page 85-87; 93pp; Japanese.
   WPI; 2002-292035/33
                                    N-PSDB; ABL50839
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Sequence 479 AA;

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                                                                                                                                                                                    203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 262
                                                                                                                                                                                                                                                    HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 322
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Length 479;
                                    Indels
100.0%; Score 1563; DB 5;
100.0%; Pred. No. 1.2e-155;
tive 0; Mismatches 0;
                                    Matches 296; Conservative
 Query Match
Best Local Similarity
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Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery; protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB; nootropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;
                                                                                                                                  Human PKB-gamma amino acid sequence.
                                   ABR57474 standard; protein; 479 AA
                                                                                                  (first entry)
                                                                                                  15-SEP-2003
RESULT 11
ABR57474
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The present invention describes a crystal of protein kinase B beta (PKBbeta) comprising (1), where (1) comprises: (a) a tetragonal space group P4-12-12 and unit cell dimensions of: a = 149.33 plus or minus of shagstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or minus 0.5 Angstrom, a = 148.40 plus or minus 0.5 Angstrom, b = 148.40 plus or minus 0.5 Angstrom, a = 149.70 plus or minus 0.5 Angstrom, c = 39.19 plus or minus 0.5 Angstrom, c = 39.90 plus or minus 0.5 Angstrom, c = 39.06 plus or minus 0.5 Angstrom, c = 39.90 plus or minus 0.5 Angstrom, c = 39.90 plus or minus 0.5 Angstrom, c = 39.06 plus or protein kinases. The crystal may also be used in minus 0.5 Angstrom a medicament for treating cancers, diabetes, erectile consultation or neurodegeneration. The present sequence represents the human PKB-gamma amino acid sequence, which is given in the exertile consultation of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New crystal of protein kinase B beta, useful for activating protein kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPBYLAPEVLEDND 322
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structural analysis; cancer; diabetes; erectile dysfunction; human;
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                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
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                                                                                                                                                                                                                                                                                                                                                                                                           Barford D, Yang J, Hemmings BA,
                                                                                                                                                                                                               14-AUG-2002; 2002WO-GB003735.
                                                                                                                                                                                                                                                               2001GB-00019860
                                                                                                                                                                                                                                                                                        01-MAY-2002; 2002GB-00009985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or a tetragonal space group.
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                    neurodegeneration
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                                                                                                                     WO2003016516-A2.
                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                        Human; protein kinase; enzyme; inhibitor; AKT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 3; 260pp; English.
                                       ADF45034 standard; protein; 479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002US-0366892P.
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                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prescott JC, Braisted A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                Human kinase AKT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003081210-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                               12-FEB-2004
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                                                                                                           ADF45034;
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ADP 45034

ADP 745034

ADP 745
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The present invention describes a composition (CI) which comprises a kinase pathway inhibitor (a) and an anti-prostate cancer compound (b). Also described: (1) identification of a mitogen-activated protein (MAP) kinase pathway inhibitor involving incubating an artivable MAP kinase pathway and selecting the molecules which inhibit the activation of the MAP kinase pathway, and (2) identification of a prostate cancer inhibitor involving incubating a cell with hydroxyflutamide and potential involving incubating a cell with hydroxyflutamide and potential inhibitor, and assaying the level of activation of MAP kinase pathway or phosphatidylinositol 3-kinase (PISK)/Akt kinase pathway. Cl has cytostatic activity, and can be used as MAP kinase inhibitor, phosphatidylinositol 3-kinase (PISK)/Akt kinase inhibitor, and androgen receptor (AR) inhibitor. Cl can be used as the presentment of prostate cancer; for identifying a mapper in the treatment of prostate cancer cancer inhibitor; and for reducing the number of prostate cancer cells in a sample. The composition Cl provides effective combination therapy as compared to prior therapies. The present sequence represents human serine/threonine kinase Akt-3, which is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKKEVIIAKDEVAHTLTESRVLKN 202
                                                                                                                                                                                                     kinase pathway inhibitor; anti-prostate cancer;
mitogen-activated protein kinase pathway inhibitor;
MAP kinase pathway inhibitor; prostate cancer inhibitor;
phosphatidylinositol 3-kinase/Akt kinase pathway;
PI3K/Akt kinase pathway; cytostatic; MAP kinase inhibitor;
PI3K/Akt kinase pathway; cytostatic; MAP kinase inhibitor;
PI3K/Akt kinase inhibitor; androgen receptor inhibitor;
PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
human; serine/threonine kinase Akt-3; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTMNDFDYLKLIGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition useful in the treatment of e.g. prostate cancer comprises a kinase pathway inhibitor and an anti-prostate cancer compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                Human serine/threonine kinase Akt-3 protein SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1563; DB 8;
100.0%; Pred. No. 1.2e-155;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 26; 118pp; English
                                         ADN71940 standard; protein; 479 AA.
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                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chang C, Lee Y, Lin W;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADN71939
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004041185-A2.
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                         12-AUG-2004
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                                                                                  ADN71940;
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RESULT 13
ADN71940
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31-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                              262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a compound for treating a cardiovascular or thrombotic disorder by combining a compound to be tested with e.g., a 9380, 9462, 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differential expression, gene therapy; aberrant vascularisation; atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia; dyslipidaemia; high blood presure; heart failure; cardiant; thrombolytic; anticoagulant; antilipaemic; hypotensive; cardiant; rac gamma Ser/Thr protein kinase; RAC-PK-gamma; BC 2.7.1.-; enzyme.
                      263 HSGKIVYRDIKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                                                                                             YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
                                                                                                                                                                       YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
  TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                    HSGKI VYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                                                                                                                                                          KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 14180 protein, a rac gamma Ser/Thr protein kinase RAC-PK-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Donoghue MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; cardiovascular disorder; thrombotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galvin KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 108; 512pp; English
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2003US-0454189P
2003US-045741P
2003US-046411P
2003US-0469041P
2003US-0478560P
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Rogrigue-Way A, Tomlinson JE,
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2003US-0445216P.
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2003US-0490660P.
2003US-0499838P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and detecting the binding.
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N-PSDB; ADQ88265.
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08-MAY-2003;
10-JUN-2003;
13-JUN-2003;
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28-JUL-2003;
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25-MAR-2003;
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cardiovascular or thrombotic disorder. Specifically, it refers to the identification of nucleic acid molecules, and the encoded proteins identification of nucleic acid molecules, and the encoded proteins thereof, which are differentially expressed in cardiovascular disease states relative to their normal expression in non-diseased tissue. The present invention describes test compounds (i.e. small molecules, peptides or antibodies) that can bind to and modulate the activity of these differentially expressed membrane-bound polypeptides, where binding is detected by a competition binding assay, immunoassay or yeast two-hybrid assay. Accordingly, pharmaceutical compositions can be developed the detected by a competition binding assay, immunoassay or yeast two-hybrid assay. Accordingly, pharmaceutical compositions can be developed at disease the developed composition in the developed at the conscious the developed composition and used via gene therapy to treat aberrant vascularisation, dyslipidaemia, high blood pressure or heart failure. As such, they achieve and cardiant activities. This polypeptide sequence is a human protein that is differentially expressed in a patient with a cardiovascular disorder, given in an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE
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(AVET ) AVENTIS PHARM PROD INC
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Pagnoni MF, Clark KL, Ivashchenko YD; Guo K,

WPI; 2001-582452/65

New nucleic acid encoding human Akt3 protein, useful for inhibiting cell death and treating myocardial infarction, ischemia reperfusion injury associated with stroke, liver damage and renal failure.

Disclosure; Page 72-73; 73pp; English.

The invention relates to human Akt3 protein (AH/PH-domain containing serine/threonine kinase, Akt) comprising a fully defined sequence (AAG78018) of 465 amino acids, its splice variant or allelic variant.

CK (AAG78018) of 465 amino acids, its splice variant or allelic variant.

Where the encoding polynucleotide hybridises under stringent conditions with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570 base pairs defined in the specification. Akt3 has cerebroprotective, noctropic, neuroprotective, antiarthritic, osteopathic, vasotropic and hepatcotropic activity, as an inhibitor of apoptosis and/or apoptosis of the setulitory region is useful for inhibition cell death. Akt3 operably linked to a regulatory region is useful for inhibition of the treating myocardial infarction or ischaemia reperfusion injury, particularly that associated infarction or ischaemia reperfusion injury, particularly that associated of the factory artery bypass grafting. Agonist of Akt3 are useful for improving theory activity during treatment of patients suffering from myocardial infarction or ischaemia reperfusion injury and inhibitors of Akt3 activity decrease tumour cell survival and result in tumour regression. Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the confarction function, improved quality of life and reduced mortality. In parine with existing heart failure, gene therapy with Akt3 reduces to process of ventricular dilation and slows down disease progression. Akt3 cell death by apoptosis, including Alzheimer's disease progression or osteoarthritis Note: The present sequence is given in the sequence of alseting but is not featured anywhere else in the specification or sequence. 

Sequence 454 AA;

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TRHPFLISLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 262 202 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 120 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 322 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240 382 9 KTWNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296 1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI Gaps ó 99.7%; Score 1558; DB 4; Length 454; 99.7%; Pred. No. 3.6e-155; tive 0; Mismatches 1; Indels ( Conservative Best Local Similarity Matches 295; Conserv 61 203 121 263 181 323 241 383 Query Match 셤 ઠે g ò g ò 유 셤 ò ð

Search completed: February 13, 2006, 06:33:40 Job time : 312 secs

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09TY9_KENLA
05ER96_BOVIN
04RLN6_TENG
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-- SIMILARITY: Contains 1 PH domain.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
V-akt murine thymona viral oncogene homolog 3 (Protein kinase B,
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Q24469
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Wallis J.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dad H.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465 AA
0868D7_AEDAE
024293_DROME
024469_DROME
07JN11_DROME
0811099_DROME
0413K9_TENDG
0519W4_CANFA
017942_CABEL
061K11_CABER
017941_CABEL
09XT77_CABEL
09XT77_CABEL
09XT45_CABEL
09XT45_CABEL
09XT45_CABEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma).
ORFNames=RP11-150L22.2-002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSVI12 HUMAN PRELIMINARY;
QSVI12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001849; PH.
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143 KTWNDFDYLKGLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN 202
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butrerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
                                                                                                                                                                                                                                     KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 466;
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                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1563; DB 2;
100.0%; Pred. No. 8.6e-96;
iive 0; Mismatches 0;
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                                                                                                                         and mouse cDNA sequences."
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ID AKT3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., McKeman K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSBDRTRFYGAEIVSALDYL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
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Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1563; DB 2; Length 465; 100.0%; Pred. No. 8.6e-96; ative 0; Mismatches 0; Indels 0
                                                                                           R SMART; SMO0233; PH; 1.—
R SMART; SMO0233; PH; 1.—
R SMART; SMO0219; S. TK X; 1.
R SMART; SMO0219; TYG; 1.
R SMART; SMO0219; TYG; 1.
R SMART; SMO0219; TYG; 1.
R PROSITE; PSSO0107; PRÖTEIN KINASE ATP; 1.
R PROSITE; PSSO0103; PH DOWAIN; 1.
R PROSITE; PSO0109; PROTEIN KINASE ST; 1.
DR PROSITE; PSO0109; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Setine/threonine-protein kinase; Transferase.
**A Setine/threonine-protein kinase; Transferase.**
**A Setine/threon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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InterPro; IPR001245; Tyr_pkinase
                      Pfam; PF00169; PH; 1.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00433; Pkinase C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q56A86 HUMAN PRELIMINARY;
Q56A86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local (
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Matches
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Production 118135; DOI=10.10'4/JDC.M104033200;
Brodbeck D., Hill M., Hemmings B.A.;
"Two splice variants of PKB gamma have different regulatory capacity depending on the presence or absence of the regulatory phosphorylation site Ser-472 in the C-terminal hydrophobic domain.";
J. Biol. Chem. 276:29550-29558(2001)
-!- FONCTION: 1GF-1 leads to the activation of AKT3, which may play a role in regulating cell survival. Capable of phosphorylating several known proteins. Truncated isoform 2/PKB gamma 1 without the second serine phosphorylation site could still be stimulated but to a lesser extent.
-!- CATALYTIC ACTIVITY: ATF + a protein = ADF + a phosphoprotein.
                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma) (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (STK-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), AND MUTAGENESIS OF THR-305 AND
                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE, AND MUTAGENESIS.

MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;

Brodbeck D., Cron P., Hemmings B.A.;

"A human protein kinase B gamma with regulatory phosphorylation sites in the activation loop and in the C-terminal hydrophobic domain.";

J. Biol. Chem. 274:9133-9136(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.; "Cloning of a novel human CDNA, STK-2, which encodes a rat serine-threonine protein kinase (STK) homolog."; but protein kinase (STK) homolog."; c the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Testis;

MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;

Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,

Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,

Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,

Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,

Wambutt R., Korn B., Klein M., Poustka A.;

"Towards a catalog of human genes and proteins: sequencing and
analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;

BEDLINE-99421751; PubMed=10491192;

Masure S., Haefner B., Wesselink J.-J., Hoefnagel E., Mortier E.,
Verhasselt P., Tuytelaars A., Gordon R., Richardson A.;
Molecular cloning, expression and characterization of the human serine/threonine kinase Akt.3.";

Eur. J. Blochem. 265:353-360(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99225329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559; Nakatani K., Sakaue H., Thompson D.A., Weigel R.J., Roth R.A.; "Identification of a human akt?" (protein kinase B gamma) which contains the regulatory serine phosphorylation site."; Biochem. Biophys. Res. Commun. 257:906-910(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11387345; DOI=10.1074/jbc.M104633200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 11:422-435(2001).
Q9Y243; Q96QV3; Q9UFP5;
                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                        Name=AKT3;
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SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after cell stimulation leading to its translocation.

ALTERNATIVE PRODUCTS:

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Q16543:CDC37; NbExp=1; IntAct=EBI-296115, EBI-295634;

INTERACTION:

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphothreonine (By similarity).
Phosphothreonine (By similarity).
YDEDGMDCMDNERRPHFPQFSYSASGRE -> CQCSDCGML
GWKK (in isoform 2).
//TIG=VSP_004947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T->D: 2-fold increase of phosphorylation steady state level, no activation after
                                      Name=2; Synonyms=PKB gamma 1;
Isoid=09Y243-1; Sequence=V5P 004947;
Isoid=09Y243-2; Sequence=V5P 004947;
ISOUS SPECIFICITY: In adult tissues, it is highly expressed in brain, lung and kidney, but weakly in heart, testis and liver. It fetal tissues, it is highly expressed in heart, and not at all in kidney.
DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC; HGNC; 393; AKT3.

RGO; GO: 00046468; Piprotein kinase activity; TAS.

RGO; GO: 00046468; Piprotein amino acid phosphorylation; TAS.

RGO; GO: 000105; P: signal transduction; TAS.

RICEPRO; IPR00199; PH.

RICEPRO; IPR00091; PH.

RICEPRO; IPR00091; Prot kinase.

REAM; PR00069; PKinase; 1.

REAM; PR00069; PKinase C; 1.

REAM; PR00013; Prot kinase; 1.

RMART; SM0013; Prot kinase; 1.

RMART; SM0013; Prot kinase; 1.

RMART; SM0013; PT K; 1.

RMART; RM0013; FT K; 1.

RMART; RM013; FT K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T->A: No activation after pervanadate
                                                                                                                                                                                                                                                                                                Phosphorylation on both serines and threonines is required for
                                                                                                                                                                                                                                                                                                                          full activity.
SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
                                                                                                                                                                                                                            kinase alpha (PI(3)K) results in its targeting to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity)
ATP (By similarity).
                                                                                                                                                                                                                                                                            PTM: Phosphorylated on threonine and serine residues.
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=PKB gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ245709; CAB53537.1; -; MRNA.
EMBL; AL117525; CAB55977.1; ALT TERM; MRNA.
EMBL; AX005799; AAF91073.1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENSG0000117020; Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF085234; AAL40392.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF124141; AAD29089.1; -; mRNA
EMBL; AF135794; AAD24196.1; -; mRNA
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HSSP; P31751; 1GZK.
SMR; Q9Y243; 1-115.
IntAct; Q9Y243; -.
Ensembl; ENSG000001170
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MOD_RES
VARSPLIC
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                                                                                                                                                                                                                                                                                                            121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                                                                                                                                                                                    263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 322
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16-0CT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RAC-gamma serine/Fireconine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133; Brodbeck D., Cron P., Hemmings B.A.; "A human protein kinase B gamma with regulatory phosphorylation sites in the activation loop and in the C-terminal hydrophobic domain."; Diol. Chem. 274:9133-9136(1999).
                                                                                                                                                                                                    1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
                                                                                                                                                                                                                                                                                                                                                               181 YGRAVDWWGLGVVMYEMMCGRLPPYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                   241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                            0; Gaps
                                                     pervanadate treatment.
S->D: 1.4-fold increase of
Desphorylation steady state level, 50%
decrease of activity after pervanadate
                                         S->A: 67% decrease of activity after
                                                                                                                                                 ; Score 1563; DB 1; Length 479;
; Pred. No. 8.9e-96;
0; Mismatches 0; Indels 0
                                                                                                                      F08BDDE6502E78FB CRC64;
pervanadate treatment.
T->A: No effect.
T->D: No effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
                                                                                                             treatment
                                                                                                                         55775 MW;
                                                                                                                                                  100.08;
                                                                                                                                                              100.08;
                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
               447
                                                                   472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                      479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
               447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKT3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Akt3;
                                                                                                                      SEQUENCE
             MUTAGEN
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                                                                   MUTAGEN
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AKT3_MOUSE
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ATP (By similarity).

Proton acceptor (By similarity).

ATP (By similarity).

Phosphothreonine (By similarity).

Phosphoserine (By similarity).

Phosphoserine (By similarity).

AUDROMOGMONERRPHPPQFSYSASGRE -> CQQSDCGML

GWNKKNDNKK (in isoform 2).

/FIId=VSP_004948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                     Name=1; Synonyms=PKB gamma;
Isold=Q9WUM6-1; Sequence=Displayed;
Name=2; Synonyms=PKB gamma 1;
Name=2; Synonyms=PKB gamma 1;
Isold=Q9WUM6-2; Sequence=PKP 004948;
TISSUE SPECIFICITY: Isoform 1 Is expressed in prostate, testis, uterus and mammary gland and isoform 2 is expressed in prostate, testis and mammary gland.
DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-kinase alpha (PI(3)K) results in its targeting to the plasma
SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after cell stimilateion leading to its translocation.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                               Phosphorylation on both sites is required for full activity. SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pfam; PF00069; Prinase; 1.
Pfam; PF00069; Prinase; 1.
Probom; PF000001; Proc Kinase; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS600107; PROTEIN KINASE ATP; 1.
PROSITE; PS600109; PROTEIN KINASE DOM; 1.
PROSITE; PS600108; ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1563; DB 1; Length 479; 100.0%; Pred. No. 8.9e-96;
                                                                                                                                                                                                                                                              PTM: Phosphorylated on threonine and serine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF124142; AAD29090.1; -; mRNA.
HSSP; P31751; 1GZK.
SMR; Q9UNG.; 1-115.
Ensembl; ENSWUSGO000019699; Mus musculus.
MGI; MGI:1345147; Akt3.
InterPro; IPR011893; PH. type.
InterPro; IPR011993; PH. type.
InterPro; IPR001994; PKinase C.
InterPro; IPR000951; Skinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
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                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 PH domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                    subfamily
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DOMAIN
NP BIND
ACT SITE
BINDING
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MOD_RES
VARSPLIC
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Matches
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                      240
                                            323 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLPELILMEDIKFPRTLSSDAKSLLSGLLI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                      YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
                                                                                                                                         Constituted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- CATALYTIC ACTIVITY: Belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: Contains | PH domain.

R EMBL; AL6529151; CAH72992.1; -; Genomic_DNA.
R EMBL; AL652999; CAH73073.1; -; Genomic_DNA.
R EMBL; AL652999; CAH72992.1; JOINED; Genomic_DNA.
R EMBL; AL652999; CAH72992.1; JOINED; Genomic_DNA.
R EMBL; AL65291721; CAH72892.1; JOINED; Genomic_DNA.
R EMBL; AL597121; CAH72892.1; JOINED; Genomic_DNA.
R EMBL; AL597121; CAH71867.1; JOINED; Genomic_DNA.
R EMBL; AL652151; CAH71867.1; JOINED; Genomic_DNA.
R EMBL; AL65299; CAH71867.1; JOINED; Genomic_DNA.
R EMBL; AL65299; CAH71867.1; JOINED; Genomic_DNA.
R EMBL; AL65299; CAH71867.1; JOINED; Genomic_DNA.
R EMBL; AC69639; CAH73073.1; JOINED; Genomic_DNA.
                                                                                                                  KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005524; F:14TP binding; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein amino acid phosphorylation; IEA.
InterPro; IPR011993; PH type.
InterPro; IPR0101993; PH type.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00219; Ser thr pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
V-akt murine thymoma viral oncogene homolog 3 (Protein kinase B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wallis J.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                  479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSG0000117020; Homo sapiens.
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00233; PH; 1.
SMART; SM00133; STK X; 1.
SMART; SM00120; S_TKC; 1.
SMART; SM00219; TYPKC; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00433; Pkinase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                gamma).
ORFNames=RP11-150L22.2-001;
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Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                             OSVTI1 HUMAN PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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CYRAIN-CD1; TISSUE-Neural Stem Cell;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Datchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield A., Schein J.B., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                          203 TRHPFLISLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 YGRAVDWWGLGVVMYEMMCGRLPPYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
                                                                                                                                                                                                                                                                                                                                                                                                    1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 438
                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                         Length 479;
                                                                                                                                                                                                                                                                                                                             Indels
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Serinase; Transferase.
Serine/threonine-protein kinase; Transferase.
SEQUENCE 479 AA; 55775 MW; F08BDDE6502E78FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGNXWO MOUSE PRELIMINARY; PRT; 479 AA.
QGNXWO;
QSJUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                     100.0%; Score 1563; DB 2; 100.0%; Pred. No. 8.9e-96;
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                         0; Mismatches
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STRAIN-CD1; TISSUE=Neural Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thymoma viral proto-oncogene 3. Name=Akt3;
                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
               ; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D49936; BAA06637.1; -; mRNA.

R HSSP, P3171; 1GZK.

R HSSP, P3171; 1GZK.

R HSSP, P3171; 1GZK.

R GO; GO:0005619; F:protein binding; IDA.

GO; GO:0005619; F:protein kinase C binding; IDA.

GO; GO:0005619; F:protein serine/threonine kinase activity; IDA.

GO; GO:0005619; F:protein serine/threonine kinase activity; IDA.

R GO; GO:0005619; F:protein serine/threonine kinase activity; IDA.

R InterPro; IPR001931; PH. Type.

InterPro; IPR001931; PH. Type.

InterPro; IPR00051; PH. 1.

R Pfam; PF00169; PH; 1.

R Pfam; PF00169; PH; 1.

R ProDom; PF00169; PH; 1.

R PROSITE; PS00101; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

M STIP-binding; Kinase; Nucleotide-binding; Phosphorylation; POMAIN; 1.

R PROSITE; PS00101; PROTEIN KINASE ST; 1.

M STIP-threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation on both sites is required for full activity. SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
ATP (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Phosphorylated on threonine and serine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphothreonine (By simi 68072CFF9DFEE876 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 1 PH domain.
                                                                                                                                                MEDLINE=96063640; PubMed=7488143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52850 MW;
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Conservative
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271 2
177 1
305 3
454 AA;
                                                                                                        NUCLEOTIDE SEQUENCE
                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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ACT SITE
BINDING
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SEQUENCE
                                              Muroidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              removed.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN 202
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
(Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KTMNDPDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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           Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

- I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
- I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
- I- SIMILARITY: Contains | PH domain.

EMBL; BC066861; AAH66861.1; -; mRNA.

EMBL; BC066861; AAH66861.1; -; mRNA.

RSR; O6NXW0; 1-115.

R MGI: 1145147; Akt3.

RGJ; GO:0004774; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004774; F:protein-tyrosine kinase activity; IEA.

RO; GO:0004774; F:protein-tyrosine kinase activity; IEA.

RO; GO:0004774; F:protein-tyrosine kinase activity; IEA.

RO; GO:0004774; F:protein-tyrosine kinase activity; IEA.

RITEPPO; IPRO10849; PH.

INTERPO; IPRO10949; PH.

INTERPO; IPRO10949; Prot kinase.

RITEPPO; IPRO10749; Prot kinase.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine/threonine-protein kinase; Transferase.
SEQUENCE 479 AA; 55657 MW; FA31AC734651B92D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Probom; PD001031; Pkinase. 1.
SMART; SM0133; PH; 1.
SWART; SM0133; PH; 1.
SWART; SM0133; STK X; 1.
SWART; SM0133; STK X; 1.
SWART; SM0139; TYKC; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP: binding; Kinase; Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
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(By similarity)

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Name=akt1;
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossar C., Sequrens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Actuald C., Skalli Z., Cattolico L., Poulann J., De Berardinis V.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Gouzy J.,
A. Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
I. Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 TRHPFLTSLKYSFQTKDRLCFVMBYVNGGELFPHLSRERVFSBDRTRFYGAEIVSALDYL 262
                                                                                                                       180
                                                                                                                                                                                     322
                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                    HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
                                                                                                                                                                                                                                                   YGRAVDWWGLGVVWYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL
                                                                                                                                                                                                                                                                                                                                                                                                              KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Estinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAP11339, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAE01011339; CAF93725.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR000719; Prot kimase.
InterPro, IPR008271; Ser thr pkin As.
InterPro, IPR002290; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001849; PH.
InterPro; IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=GSTENG00009507001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q4T057 TETNG PRELIMINARY;
Q4T057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
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                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 KTWNDPDYLKLLGKGTFGKVILVKEKASGTYYAMKILKKEVIIAKDEVAHTLTESRVLKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 LDKDGHIKITDFGLCKEGITDTATMKTFCGTPEYLAPEVLEDNDYGRGVDWWGLGVVMYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 MACGRIPFYNQDHEKLFELILMEBIKFPRTLSADAKSILSGLLIKDPNKRLGGGPDDAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SLKYSFQTKDRLCFVMEYVNGGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 ------LFFHLSRERVFSEDRTRFYGAEIVSALDYLHSGKIVYRDLKLENLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 LDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDYGRAVDWWGLGVVMYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 MMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLGGGPDDAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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-!- GATALYTIC ACTIVITY: ATP + a protein = App + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: Contains 1 PH domain.
EMBL; AF039943; AAB94767.1; -; mRNA.
HSSP; P31749; 1H10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              523 AA; 60242 MW; D2FC6BED3B92090F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 IMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Serine/threonine protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 IMRHSFFSTIDWQDLYDKKLVPPFQPQVTSETDTRYFDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%; Score 1428; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.5%; Pred. No. 9.1e-87; ive 8; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase, Transferase.
NON TER 523 523
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                 Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF0013; Pkinase; 1.
Probom; PD00001; Prot kinase; 1.
SMART; SM00233; PH; 1.
SMART; SM00133; STK X; 1.
SMART; SM00220; STKZ; 1.
SMART; SM0020; STKZ; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
InterPro; IPR001245; Tyr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TRHPFLT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O57513 CHICK PRELIMINARY; 057513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.5
Matches 277; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                    523
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147 TWNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNS 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 SGK-IVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 SEKNVVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDND 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGRAVDWWGLGVVMYEMMCGRLPPYNQDHEKLFELILMEDIKPPRTLSSDAKSLLSGLLI 240
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:000648; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001849; PH.
InterPro; IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 481;
                                         InterPro; IRRO00501; Firinge C.
InterPro; IRRO00519; Prot kinase.
InterPro; IRRO00219; Prot kinase.
InterPro; IRRO002209; Ser_thr_pkinase.
InterPro; IRRO002209; Ser_thr_pkinase.
Ffam; PP00169; PH; 1.
R Ffam; PP00169; PH; 1.
R Fram; PP00109; Prinase; 1.
R SWART; SW0013; PH; 1.
R SWART; SW0023; PH; 1.
R SWART; SW0023; FH; 2.
R SWART; SW0013; FH; 3.
R SWART; SW0013; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.6%; Score 1416.5; DB 88.9%; Pred. No. 4.8e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
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10-WAY-2005 (TrEMBLrel. 30, Last seq
10-WAY-2005 (TrEMBLrel. 30, Last ann
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QSER96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 263; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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                    원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKNAVVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDND 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGK-IVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLSPEAKSLLSGLLK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHPFLTSLKYSFQTKDRLCPVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersen C.B., Sakaue H., Roth R.A., Conti M.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF317655, AAG59601.1; -; mRNA. HSSP; P31751; 1MRY. SMR; Q98TY9; 1-116. GO; Go:0006524; F:ATP binding; IEA. GO; Go:0004674; F:protein serine/threonine kinase activity; IEA. GO; GO:0006468; P:protein amino acid phosphorylation; IEA. InterPro; IFR001849; PH.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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                                                                                                                                                      InterPro; IPRO1993; PH. type.

R InterPro; IPR00961; PkInase_C.
R InterPro; IPR000251; Ser_thr_pkinase.
R InterPro; IPR002290; Ser_thr_pkinase.
R InterPro; IPR002290; Ser_thr_pkinase.
R InterPro; IPR002290; Ser_thr_pkinase.
R Pfam; PF00169; Pkinase C; 1.
R Pfam; PF00169; Pkinase C; 1.
R Pfam; PF001001; Prot_kinase; 1.
R SMART; SM00131; Pki, 1.
R SMART; SM00131; Pki, 1.
R SMART; SM00123; Pki, 1.
R PR05ITE; PS00101; PR0TEIN KINASE DOM; 1.
R PR05ITE; PS00108; RN0TEIN KINASE DOM; 1.
R PR05ITE; PS00108; PR0TEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.9%; Score 1420.5; DB 3 89.5%; Pred. No. 2.6e-86; ative 18; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481
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Q98TY9;
                                                                                                                             InterPro, IPR001849; PH.
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NUCLEOTIDE SEQUENCE.
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g ò d ઠે 엄 8 q 8 61

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258; Conservative
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                A THE SECOND OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 YGRAVDWWGLGVVMYSMWCGRLPFYNQDHEKLFELILMEEIRFPRTLSPEAKSLLSGLLK 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis (Green puffer).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nuclear protein; Nucleotide-binding; Scrina-fracenine-protein kinase; Transferase.
SEQUENCE 480 AA; 55748 MW; 152E6613C4E6ED5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
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13.5EP-2005 (TrEMBLrel. 31, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.7%; Score 1402.5; DB 2
88.5%; Pred. No. 4.1e-85;
tive 19; Mismatches 14;
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001290; Ser-thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; Pr00169; PH; 1.
Pfam; Pr00069; Pkinase; 1.
Pfam; Pr00069; Pkinase; 1.
Pram; Pr000001; Prot kinase; 1.
SWART; SW00133; Pkinas; 1.
SWART; SW00213; PK; 1.
SWART; SW00219; TYK; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q4RLN6_TETNG PRELIMINARY;
Q4RLN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 88.5 tes 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment
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Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFBLILMEDIKFPRTLSSDAKSLLSGLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B in
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                                                                                                                                                                                                                                                                                                                                                                                                  MPF (By similarity).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIBUNIT: Forms a stable but non-covalent complex with cyclin B in the complex belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: Contains 1 PH domain.
R EMBL; CAAE01015019; CAG10696.1; -; Genomic_DNA.
R InterPro; IPR000353; FHA.
R InterPro; IPR00353; FHA.
R InterPro; IPR003519; Prinase.
R InterPro; IPR003519; Prot. Kinase.
R InterPro; IPR003511; Ser_thr_pkin_AS.
R InterPro; IPR002590; Ser_thr_pkin_AS.
R InterPro; IPR001591; Tyr_pkinase.
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 1893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1893 AA; 210868 MW; 7F9B5064C2BC2632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.3%; Score 1396.5; DB 2
87.2%; Pred. No. 4.6e-84;
iive 23; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine/threonine-protein kinase; Transferase.
NON TER 1
NON TER 1893 1893
SEQÜENCE 1893 AA; 210868 MW; 7F9BSO64C2BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00498; FHA; 1.
Pfam; PF00498; FHA; 1.
Pfam; PF00499; PH; 1.
Pfam; PF00439; PKinase; 1.
ProDom; PD000001; Prot_Kinase; 1.
SMART; SM00240; FHA; 1.
SMART; SM00233; PH; 1.
SMART; SM00213; PH; 1.
SMART; SM00213; PH; 1.
SMART; SM00219; TYK¢; 1.
SMART; SM00219; TYK¢; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS500107; PROTEIN KINASE DOM; 1.
PROSITE; PS500108; PROTEIN KINASE DOM; 1.
PROSITE; PS500108; PROTEIN KINASE ST; 1.
PROSITE; PS500108; PROTEIN KINASE ST; 1.
                                                                       the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      480 AA;
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        PS50003;
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156
274
179
308
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ACT SITE
BINDING
MOD RES
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MOD_RES
SEQUENCE
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Best Local S
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DD11D
DD1D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
  364 KDPMQRLGGGPDDAKEIMQHKFFAGIEWKDVYEKKLVPPFKPQVTSETDTRYFDEE 419
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required for full activity. Ser-473 is dephosphorylated by PHLPP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005515; F:protein binding; IDA.
GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0006916; P:anti-apoptoeis; IMP.
GO; GO:0030307; P:positive regulation of cell growth; IDA.
GO; GO:0007165; P:signal transduction; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ensembl; ENSRNOG00000028629; Rattus norvegicus RGD; 2081; Aktl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 PH domain.
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InterPro; IPR000961; Pkinase C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkin_AS.
Pfam; PF00169; PH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D30040; BAA06279.1; -; mRNA.
PIR; JC2437; JC2437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; Pkinase; 1.

Pfam; PF00433; Pkinase_C; 1.

ProDom; PD000001; Prot_Kinase; 1.

SMART; SM00233; PH; 1.

SMART; SM00133; S TK X; 1.

SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95091823; PubMed=7999118;
                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seqn
13-SEP-2005 (Rel. 48, Last ann
                                                                                                                                                                                                                                                                                                                      (Protein kinase B) (PKB).
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P31749; 1H10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P47196; 3-121
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                                                                                                                                          AKT1 RAT
P47196;
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                                                                                     RESULT 13
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X REDLINE=2238825; PubMed=1247793; DOI=10.1073/pnas.242603899;
A StraueBerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habteh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH 121
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphoserine (by ILK1) (By similarity). Phosphotyrosine (By similarity). SDCAAE7134366D04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 480;
                                                                                                                                                                                                                           Protein kinase.

ATP (By similarity).

Proton acceptor (By similarity).

ATP (By similarity).

Phosphothreonine (by PDPK1) (By
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
10-MAX-2005 (TrEMBLrel. 30, Last annotation update)
Thymoma viral proto-oncogene 1 (Protein kinase B-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%; Score 1394.5; DB 187.8%; Pred. No. 1.4e-84;
                                                                                                                                                     Serine/threonine-protein kinase; Transferase.
DOMAIN 150 408 Protein kinase.
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QGGSA6;
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Name=V-AKT;
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Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones B.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22803305; PubMed=12783884; DOI=10.1074/jbc.M302847200; M3ng Z.Z., Tschopp O., Hemmings-Mieszczak M., Feng J., Brodbeck D. Perentes E., Hemmings B.A.; B.A.; "Protein Kinase B{alpha}/Aktl Regulates Placental Development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang Z., Hemmings B.A.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: Contains 1 PH domain.
EMBL; AF534134; AAN04036.1; -; Genomic_DNA.
EMBL; BC066018; AAH66018.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ensembl; ENSWUSGO000001729; Mus musculus.

Ensembl; ENSWUSGO000001729; Mus musculus.

Ensembl; ENSWUSGO0000001729; Mus musculus.

Ensembl; ENSWUSGO000001729; Mus musculus.

Ensembl; ENSWUSGO000001729; Mus musculus.

GO; GO:0000513; C:cytoplasm; IDA.

GO; GO:0000515; F:protein binding; IPI.

GO; GO:0000515; P:protein binding; IPI.

GO; GO:0000515; P:protein Ensemption in DA.

GO; GO:0000515; P:protein Ensemption of apoptosis; IDA.

GO; GO:00007281; P:germ cell development; IDA.

GO; GO:00007881; P:germ cell development; IDA.

GO; GO:00016468; P:protein amino of apoptosis; IDA.

GO; GO:00016468; P:protein amino acid phosphorylation; IDA.

GO; GO:0016668; P:protein catabolism; IDA.

GO; GO:001668; P:protein ubiquitination; IDA.
                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN-ESTBL/6; TISSUB-Brain;
Director MGC Project;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 480 AA; 55707 MW; 98DF28E5EFE03730 CRC64;
                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO: 0003013; C: Cytoplasm; 1DA.
GO; GO: 0003819; C: Spindle; IDA.
GO; GO: 0005515; F: Protein binding; IPA.
GO; GO: 00042640; P: Protein binding; IPA.
GO; GO: 00042640; P: Protein binding; IPI.
GO; GO: 00042640; P: Protein kinase activity;
GO; GO: 0006515; P: Protein kinase activity;
GO; GO: 0006515; P: Protein kinase activity;
GO; GO: 0006515; P: Protein mino acid phosph
GO; GO: 0006515; P: Protein amino acid phosph
GO; GO: 0001656; P: Protein amino acid phosph
GO; GO: 0016567; P: Protein amino acid phosph
GO; GO: 01016567; P: Protein amino acid phosph
GO; GO: 01016667; P: Protein am
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J. Biol. Chem. 278:32124-32131(2003).
[4]
                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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Gaps

1,

15, Indels

; Pred. No. 1.4e-84; 20; Mismatches 15

87.8%;

Matches 260; Conservative

Best Local Similarity

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                    146 TWINEFEYLKLIGKGTFGKVILVXEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNS 205
                                                                              RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH 121
                                                                                                206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAE1VSALDYLH 265
                                                                                                                                                      SGK-IVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND 180
                                                                                                                                                                          266 SEKNYVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPBYLAPEVLEDND 325
                                                                                                                                                                                                                                  181 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
                                                                                                                                                                                                                                                    326 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPEAKSLLSGLLK 385
    61
TWNDFDYLKCLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
                                                                                                                                                                                                                                                                                                          241 KDPNKRLGGGPDDAKEIMRHSFRSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
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                                                                                                                                                                                                                                                                                                                                polyprotein. -- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
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MEDLINE=92022574; PubMed=1833819;
Bellacosa A., Testa J.R., Staal S.P., Tsichlis P.N.;
Ballacosa A. testa J.R., et and an St. att, encoding a serine-threonine kinase containing an SH2-like region.";
Science 254:274-277(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: Autophosphorylated on threonine and serine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-SEP-2005 (Rel. 48, Last annotation update)
AKT kinase transforming protein (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M80675; AAA42545.1; -; Genomic_DNA.
HSSP; P31749; 1H10.
SMR; P31749; 1H10.
InterPro; 1PR001849; PH.
InterPro; 1PR001849; PH.
InterPro; 1PR001993; PH.
InterPro; 1PR000561; Pkinase C.
InterPro; 1PR000271; Ser thr pkinase.
InterPro; 1PR002290; Ser thr pkinase.
InterPro; 1PR002290; Ser thr pkinase.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00069; Pkinase; 1.
Pfam; PF00069; Pkinase; 1.
SMART; SM00231; PH; 1.
SMART; SM00233; PH; 1.
PROSITE; PS50013; PH DOMAIN; 1.
PROSITE; PS50011; PROTEIN KINASE APP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              501 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKT8 murine leukemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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NCBI_TaxID=11790;
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167 TMNEFEYLKLLGKKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLQNS 226
                                                                                                                                                                                                                                                                    227 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLH 286
                                                                                                                                                                                                                                                     RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGABIVSALDYLH 121
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                                                                                                                                                                                                                                                                                                                                                                                                            KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPPKPQVTSETDTRYFDEE 296
                                                                                                                                                                            1; Gaps
PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Nuclectide-binding; Oncogene; Phosphorylation; Serine/threonine-protein kinase; Transferase.

DOMAIN 26 129 PH.

PH. POMAIN 171 429 Protein kinase.

NP BIND 177 185 ATP (By similarity).

ACT SITE 295 295 Proton acceptor (By similarity).

BINDING 200 200 ATP (By similarity).
                                             PH.
Procein kinase.
Procein kinase.
ATP (By similarity).
ATP (By similarity).
ATP (By similarity).
Phosphotyrosine (By similarity).
W; SAEPDESSCD42F773. CRC64;
                                                                                                                                               89.2%; Score 1394.5; DB 1; Length 501; 87.8%; Pred. No. 1.5e-84; Ative 20; Mismatches 15; Indels 1;
                                                                                                                         57870 MW;
                                                                                                                                               Query Match
Best Local Similarity 87.8*
Matches 260; Conservative
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129
185
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171 4
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295 2
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SEQUENCE
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Search completed: February 13, 2006, 06:40:49 Job time : 429 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                        Copyright
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sw model - protein search, using OM protein Run on:

Pebruary 13, 2006, 06:33:54 ; Search time 73 Seconds
(without alignments)
390.139 Million cell updates/sec

US-10-601-311-1\_COPY\_143\_438

1563 1 KTWANDFDYLKLLGKGTFGKV.....VPPFKPQVTSETDTRYFDEE 296 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pir1:\*
1: pir2:\*
1: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query re Match Length DB	DB	ID	Description
7	1563	100.0	462	-	T17287	protein kinas
7	1563	100.0		-	A59380	protein kinas
М	1558	99.7		Н	JC4345	protein kinas
4	1394.5	89.2		Н	JC2437	protein kinas
ហ	1394.5	89.2		Н	833364	protein kinas
9	1394.5	89.2		-	A40831	gag-akt polyr
7	1393.5	89.2		-	A39360	protein kinas
80	1391	89.0	481	н	A46288	protein kinas
σ	1378.5	88.2		Н	862117	protein kinas
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SUMMARIES	QI	T17287	A59380	JC4345	JC2437	S33364	A40831	A39360	A46288	862117	JC2438	A55888	T43233	T43232	T21523	T43234	A48094	A23690	S29478	KIRBCE	KIMSCE	S28942	A46079	A39666	KIRTCE	861917	T43051	835362	T22856	KIHUC1
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	Score	1563	1563	1558	1394.5	1394.5	1394.5	1393.5	1391	1378.5	1378	1240	1118.5	1098	1032	1027	857	826	822	819.5	819.5	819.5	819	815	811.5	811	807	802	800.5	799.5
	sult No.	-	7	٣	4	ហ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

181 YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240

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B32392	KIRBC1	A53530	KIRTC1	861918	T28666	S37955	KIBOC	KIBOC2	KIHUC2	\$11213	T26334	KIRBC	A38578	KIHUCA	KIMSCA
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## ALIGNMENTS

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Tilizary transe (BC 2.7.1.37) akt3 short splice form - human protein kinase (BC 2.7.1.37) akt3 short splice form - human N.Alterante names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protein C.Species: Homo sapiens (man) (man
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A; Residues: 1-480 <KON>
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                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: A59380; A59379
R;Brodbeck, D.; Cron, P.; Hemmings, B.A.
J. Biol. Chem. 274, 9133-9136, 1599
A;Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the actiA;Reference number: A59380; MUID:99194749; PMID:10092583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335E8; GB:AAD29089; NID:g4757579; PI R;MaBure, S.; Haefner, B.; Wesselink, J.J.; Hoefnagel, E.; Mortier, E.; Verhasselt, P.; Briochem. 265, 353-360, 1999
A;Title: Molecular cloning, expression and characterization of the human serine/threonin A;Reference number: A59379; MUID:99421751; PMID:10491192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A pescription: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A; Pathway: signal transduction pathways regulating various processes
C; Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology, protein C; Keywords: ATP; autophosphorylation; phosphorotein; phosphotransferase; proto-oncogene F; 7-108/Domain: pleckstrin repeat homology «KIN»
F; 149,408/Domain: protein kinase homology «KIN»
F; 157-165/Region: protein kinase ATP-binding motif
F; 77/Active site: Lys #status predicted
F; 73/54tinding site: phosphate (Thr) (covalent) #status predicted
F; 74/4/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
                                                                                                                                                                                                                                            protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] – human
N/Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prot
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203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYL 262
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                                                                                                    1 KTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKN
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                                                                         241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE
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A;Cross-references: GDB:9954867
A;Map position: 1q44-1q44
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Matches 296; Conservative
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A,Molecule type: DNA
A,Residues: 1-479 <MAS>
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A;Status: preliminary
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protein kinase (EC 2.7.1.37) akt3 [validated] - rat
NyAlternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protein
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: JC4435
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; Ki
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase
C subspecies and beta gamma subunits of g proteins.
A;Reference number: JC4345; MUID:96063640; PMID:7488143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A; Destribwy: aignal transduction pathways regulating various processes
C; Superfamily: RAC serine/threonine-protein kinase; plackstrin repeat homology; protein b; C; Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase. Lois/Domain: pleckstrin repeat homology «PLX»
F; 146-405/Domain: protein kinase homology «RIX»
F; 146-405/Domain: protein kinase homology «KIX»
F; 154-162/Region: protein kinase ATP-binding motif
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NyAlternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protein Cippecies: Rattus norvegicus (Norway rat)
Cippecies: Rattus norvegicus (Norway rat)
Cipate: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
Cipate: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
Rikonishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association
A;Reference number: JC2437; MUID:95091823; PMID:7999118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PII A;Experimental source: brain C;Function:
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C, Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein }
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260; Conservative
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C.Jate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C.Jate: 10-Sep-1999 #sequence_revision and chromosomal mapping of c-akt: relationship to v-akt a A.Faference number: 33354; MUID:93173519; PMID:8437858
A.Faterence number: 33354; MUID:93173519; PMID:8437858
A.Faterence number: 33354
A.Faterence number: 533564
A.Faterence number: 63697
A.Faterence number: 63607
A.Faterence number: 63697
A.Faterence number: 6367
A.Faterence
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F14-106/Domain: pleckstrin repeat homology <PLK>F14-106/Domain: pleckstrin repeat homology <PLK>F15-164/Domain: protein kinase homology <RIN>F156-164/Region: protein kinase ATP-binding motif F156-164/Region: protein kinase ATP-binding motif F159/Binding site: Lya #status predicted F150/Binding site: Lya #status predicted F150/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki F1473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
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                                                                                                                                                                                                                                                                                                                                                      TWNEFEYLKLIGKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVAHTLTENRVLONS 205
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                                                                                                                                                                                                                 DB 1; Length 480;
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llarity 87.8%; Pred. No. 3.8e-56;
Conservative 20; Mismatches 15
                                                                                                                                                                                                                 Score 1394.5; DB Pred. No. 3.8e-56;
                                                                                                                                                                                        89.2%; Scur-
87.8%; Pred. No. 5...
**** 20; Mismatches
                                                                                                                                                                                                                                          Best_Local Similarity 87.89
Matches 260; Conservative
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A403ca

A403ca and the core protein p30; core protein p15; inner coat protein p12; kine C; Species: AKT8 murine leukemia virus C; Date: 12-Peb-1933 #sequence_revision 12-May-1994 #text_change 31-Dec-2004 C; Date: 12-Peb-1933 #sequence_revision 12-May-1994 #text_change 31-Dec-2004 C; Date: 12-Peb-1933 #sequence_revision 12-Peb-1933 #sequence as the containing an SH; A; Reference number: A40831; MulD:92022574; PMID:1833819
A; Recession: A40831
A; Residues: 1-262 ABEL-A; A; Residues: 1-262 ABEL-A; A; Residues: 252-763 ABEL-A; A; Residues: A; Residu
                                                                                                                                                                                                                                         325
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    121
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SGK-IVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDND
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87.8%; Pred. No. 5.5e-56;
ive 20; Mismatches 15; 1
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F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experimer
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C, Function:
                                                                                                                                                  Conservative
                                                                                                           Local Similarity
Les 260; Conserv
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A; Residues: 1-481 <CHE>
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Matches 255; Conser
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                                                                                                                   Best Loca
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A; Residues: 63-70, 'TESSSAACSGPLSSNAPSWWRLLRSGGVDNRHPDCGRRPQ','EAGGGGDGLPVGLTQRQLRGRRDGGV
A; Residues: 63-70, 'TESSSAACSGPLSSNAPSWWRLLRSGGVDNRHPDCGRRPQ','EAGGGGDGLPVGLTQRQLRGRRDGGV
A; Cross=references: UNIPARC:UP100001725AC; EMBL.K61037
A; Note: this sequence has been revised in reference 524423
B; Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming
EMBO J. 15, 6541-6551, 1996
A; Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
A; Reference number: A64192; MUD:9713284; PMID:8978681
A; Contents: annotation; phosphorylation sites
A; Contents: annotation; phosphorylation sites
A; Contents: Activation by A.C.
J. Biol. Chem. 275, 8271-8274, 2000
A; Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PD
A; Reference number: A64193; MUD:20187529; PMID:10722653
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F; 4-106/Domain: protein kinase homology <PLKs
F; 1-106/Domain: protein kinase ATP-binding motif
F; 1-106/Region: protein kinase ATP-binding motif
F; 1-106/Region: protein kinase ATP-binding motif
F; 1-106/Region: protein kinase ATP-binding motif
F; 1-108/Binding site: Lys #status predicted
F; 1-108/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein kin
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A;Residues: 63-70,'TPSSSAACSGPLSSNAPSWMRLLRSGGVDNRHPDCGRRPQ','EAGGGGDGLPVGLTQRQLRGRRDGGV
A;Cross-references: UNIPARC:UP100001725AB; EMBL.X61037
A;Nores-the nucleotide sequence was submitted to the EMBL Data Library, July 1991
A;Note: this sequence has been revised in reference $24423
R;Coffer, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Contents: annotation; autophosphorylation site
C;Comment: Aktl is ubiquitous as an inactive multimeric complex. It binds phosphatidyl-3
nt protein kinase 1 complex. Aktl can then autophosphorylate and become fully active.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes including insulin a
                                                                                                                                                         prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-480 <JON>
A;Cross-references: UNIPROT:P31749; UNIPARC:UP1000002E75B; GB:M63167; NID:g190827; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinas
A;Reference number: S17999; MUID:92037600; PMID:1718748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 63-172, A',175-201, O',203-211, R',213-245, A',247-408, T',410-475, P',477,
A): Cross-references: UNIPARC:UP1000016AEB1; EMBL:X61037; NID:35480; PIDN:CRA43372.1; PI
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
A; Note: this a revision to the sequence from reference S17999
                                                                                                                                                                                                                                                                                                                                                                         ğ
                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence revision 12-May-1994 #text_change 16-Aug-2004
C;Accession: A33360; 836389; $$18000; $$20836
R;Jones, P.F.; Jakubowicz, T.; Pitcossi, F.J.; Maurer, F.; Hemmings, B.A.
Proc. Natl. Acad. $$21. US. A. 88; 4171-4175; 1991
A;Ttle: Molecular cloning and identification of a serine/threonine protein kinase
A;Reference number: A39360; MUID:91239529; PMID:1851997
                                                                                                                                      N'Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: $36389
A,Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:1533586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Coffer, P.
submitted to the EMBL Data Library, July 1991
A;Reference number: S20836
                                                                                                    [validated]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: S18000
A,Status: nucleic acid sequence not shown
                                                                                                               akt1
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A Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A Pathway: algnal transduction pathways regulating various processes (Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein ) C; Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinacles/tof/Domain: pleckstrin repeat homology vELx> F;150-409/Domain: protein kinase homology vELx> F;150-409/Domain: protein kinase homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: A6628
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; TE
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9211, 1992
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/thm
A;Reference number: A46288; MUID:93028445; PMID:1409633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or peptidyl-threonine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas. C;Genetics:
A;Gene: GDB:AKT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase (EC 2.7.1.37) akt2 - human
NAILernate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 SEKOVVYRDLKLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPEYLAPEVLEDND 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGRAVDWWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
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                                                                                                                                                                                                  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH 121
                                                                                                                                                                                                                                                                                                                                                                                 206 RHPFLTALKYSFQTHDRLCFVMBYANGGELFFHLSRERVFSEDRARFYGAEIVSALDYLH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 YGRAVDWWGLGVVWYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPEAKSLLSGLLK 385
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                                                                                                                                                      2 TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE 296
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   Length 480;
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DB 1;
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llarity 86.4%; Pred. No. 5.4e-56;
Conservative 23; Mismatches 17;
89.2%; Score 1393.5; DB 87.8%; Pred. No. 4.2e-56; iive 20; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:135660; OMIM:164731
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protein kinase (EC 2.7.1.37) akt2 [validated] - rat
NyAlternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein
C;pecies: Rattus norregicus (Norway rat)
C;baccession: JC2438
Rikonishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
B;cohen: Biophys. Res. Commun. 205, 817-825, 1994
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association
A;Reference number: JC2437; MUID:95091823; PMID:7999118
A;Accession: JC2438
A;Accession: JC2437
A;Accession: JC2437
A;Accession: JC2438
A;Accession: JC2438
A;Accession: JC2438
A;Accession: JC2438
A;Accession: JC2438
A;Accession: JC2438
A;Accession: JC2437
A;Accession: JC2438
A;Accession: JC2437
A;Ac
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NyAlternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase RAC
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: D.O.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A55888
R;Andjelkovic, M; Jones, P.F.; Grossniklaus, U; Cron, P.; Schier, A.F.; Dick, M.; Bilbe
A;Title: Developmental regulation of expression and activity of multiple forms of the Drc
A;Reference number: A55888
A;Accession: A55888
A;Accession: A55888
A;Accession: A55888
A;Accession A55888
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                                                                                                           241 KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253; Conservative
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A; Cotagen: S24433
A; Status: nucleic acid sequence not shown
A; Residues: 70-78, NV, 80-145 < COW
A; Status: nucleic acid sequence from reference S17999
B; Coffer, P. D.; Woodgett, U, G. R.
Bur. J. Biochem. 201, 475-481, 1991
A; Title: Molecular cloning and characterisation of a novel putative protein-serine kinas
A; Reference number: S1799; MUID:92037600; PMID:1718748
A; Reference number: S1799; MUID:92037600; PMID:1718748
A; Reference number: S1799; MUID:92037600; PMID:1718748
A; Residues: 170, 'TPSSSAACSGPRSSSARSTWRRPRSGGVDRRHPDGGRRAQEAGGGDDGLPVGLTRRELGGRGDGGVAGQP
A; Residues: 170, 'TPSSSAACSGPRSSSARSTWRRPRSGGVDRRHPDGGRRAQEAGGGDDGLPVGLTRRELGGRGDGGVAGQP
A; Residues: UNPARC:UPT00001725AB; EMBL:K61036
A; Rote: this sequence has been revised in references $62117 and $24423
C; Punction: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin-A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin-C; Reywords: ATP; autophosphorylation, phosphoprotein; phosphotransferase; proto-oncogene F; 4106/Domain: precein kinase homology < KIN>F; 148-408/Domain: precein kinase homology < KIN>F; 148-408/Domain: protein kinase kite: phosphate (Ser) (covalent) (by phosphoinositide-dependent protein k; F; 319/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
F; 313/Binding site: phosphate (Ser) (covalent) (by autophosphorylation)
                                                                                                                                                                                                                                                                                                                                                                                          Direction kinase (EC 2.7.1.37) akt1 [similarity] - bovine
NiAlternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C.Species: Bos primits taurus (cattle)
C.Species: Bos primits taurus (cattle)
C.Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C.Accession: S62117; S24423; S17999; S15714; S36388
R.Coffer, P.J.; Woodgett, J.R.
Submitted to the BMBL Data Library, December 1991
A.Reference number: S62117
A.Residues: 1-480 cCDS-
A.Residues: 1-480 cCDS-
A.Coss-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PIDN:C
A.Roce: P.J.; Woodgett, J.R.
B.Coffer, P.J.; Woodgett, J.R.
B.Coffer, P.J.; Woodgett, J.R.
B.Coffer, D.J.; Woodgett, J.R.
A.Reference number: S24423; MUID:92249329; PMID:1533586
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                                                                           GRAVDWWGLGVVWYEMMCGRLPFYNQDHERLFELILMEEIRPPRTLSPEAKSLLAGLLKK
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                                                                                                                                                                                                                                           442
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A pescription: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A; Pathway: signal transduction pathways regulating metabolism, development, and longevity c): Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein b; F;14-116/Domain: pleckstrin repeat homology <PLK>
F;191-455/Domain: pleckstrin repeat homology <PLK>
F;191-455/Domain: protein kinase homology <KIN>
F;192-207/Region: protein kinase APP-binding motif
F;222/Active site: Lys #status predicted
F;355/Binding site: phosphate (Thr) (covalent) #status predicted
F;522/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-541 <MIL>
A;Residues: 1-541 <MIL>
A;Residues: 1-541 <MIL>
A;Cross-references: UNIPARC:UPI0000080469; EMBL:Z73969; PIDN:CAA98240.1; GSPDB:GN00023; C
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A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 318/3; 361/3; 482/3
                                                                                                                                                                                                                                                                                                                           71.6%; Score 1118.5; DB 1; Length 68.7%; Pred. No. 9.7e-44; ive 40; Mismatches 49; Indels
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A,Status: translated from GB/EMBL/DDBJ
Molecule type: mRNA
A,Residues: 1-541 <PAR>
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Matches 206; Conservative
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                                                                                               A,Cunser references: FlyBase: FBgn0013324
A,Strart codon: ACG
A,Introns: 261/3; 327/3; 457/3; 535/3; 584/3
A,Strart codon: ACG
A,Introns: 261/3; 327/3; 457/3; 535/3; 584/3
C,Function:
C,Function: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A,Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A,Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C,Superfamily: RAC serine/threonin-protein phosphortein; phosphotransferase; serine/threonin
C,Keywords: ATP; autophosphorylation; phosphortein; phosphotransferase; serine/threonin
C,Keywords: ATP; autophosphorylation; phosphorylation motif
F,242-280/Region: protein kinase ATP-binding motif
F,255/Active site: Lys #status predicted
F,423/Binding site: phosphate (Thr) (covalent) #status predicted
F,586/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte
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A)Reference number: 219092
A)Reference number: 219092
A)Status: translated from GB/EMBL/DDBJ
A)Rolecule type: DNA
A)Residues: 1-546 < WILb>A)Cross-references: UNIPARC: UPI00000756DF; EMBL: Z73969; PIDN: CAA98238.1; GSPDB: GN00023;
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A;Cross-references: UNIPROT:Q17942; UNIPARC:UPI00000756DF; EMBL:AF072380; NID:g3694830;
R;McMurray, A.
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                         A; Cross-references: UNIPROT: Q24469; UNIPARC: UPI00000866BE; GB: X83510
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A;Residues: 1-611 <AND>
                                                                              A;Gene: FlyBase:RacPK
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ò 원 A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A; Description: signal transduction pathways regulating metabolism, development, and longevity C; Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein F; Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotransi F; 14-116/Domain: pleckstrin repeat homology < PLK>
F; 191-450/Domain: protein kinase homology < KIN>

A,Map position: 5 A,Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 323/3; 366/3; 487/3

A;Experimental source: clone C12D8

A;Gene: akt-1; C12D8.10

Genetics:

us-10-601-311-1

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194; Conservative
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A; Map position: X
A; Map position: 32/2; 68/3; 135/3; 175/3; 241/3; 285/2; 305/3; 348/3; 469/3
C; Punction:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin-pathways regulating metabolism, development, and longevit C; Superfamily: RAC serine/threonine-protein Kinase; plecketrin repeat homology; protein C; Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans F; 11-113/Domain: plecketrin repeat homology <PLK-F; 11-113/Domain: plecketrin repeat homology <PLK-F; 178-437/Domain: protein Kinase homology <PLK-F; 186-194/Region: protein Kinase ATP-binding motif
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F;199-207/Region: protein kinase ATP-binding motif
$222/Active site: Lys #status predicted
F;350/Binding site: phosphate (Thr) (covalent) #status predicted
F;517/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Caenorhabditis elegar
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A;Residues: 1-528 <WI2>
A;Zross-references: UNIPARC:UPI000076045; EMBL:Z92837; PIDN:CAB07403.1; GSPDB:GN00028; A;Experimental source: clone R03E1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-528 <WIL>
Cross-references: UNIPROT:Q9XTG7; UNIPARC:UP10000076045; EMBL:AL031621; PIDN:CAA20936.
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                                                                                                                                                                                           61
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                                                                                                                                                                                                                 309 RCDIVYRDMKLENLLLDKDCHIKIADFGLCKEEISFGDKTSTFCGTPEYLAPEVLDDHDY
                                                                                                                                                                                                                                                                                                                                                                                                                                          RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH
                                                                                                                                                                                                                                                                                                    SGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDY
                                                                                                                                                                                           TMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILKKEVIIAKDEVAHTLTESRVLKNT
                                                                                                                                                  Gaps
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                                                                                                        DB 1; Length 541;
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;337/Binding site: phosphate (Thr) (covalent) #status predicted
;505/Binding site: phosphate (Ser) (covalent) (by autophosphory)
                                                                                                                                                  54; Indels
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Pred. No. 7.1e-40;
                                                                                                                              8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, September 1998
                                                                                                                                                  39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, March 1997
A;Reference number: 219812
A;Accession: T23878
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                        70.2%; Score 1098; 68.5%; Pred. No. 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: 219434
A; Accession: T11523
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-528 <WILD-A; Cross-references: UNIPROT: 09XTG7; UNIPA
A; Experimental source: clone F28H6
R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-528 <WI2>
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65.8%;
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Matches 202; Conservative
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Best Local Similarity
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protein kinase (EC 2.7.1.37) akt-2 short splice form [similarity] - Caenorhabditis elegar N;Alternate names: PKB; protein kinase B C;Species: Caenorhabditis elegans C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004 C;Accession: T43234 R;Paradis, S; Ruvkun, G Genes Dev. 12, 2488-2498, 1998 A;PKB transduces insulin receptor-like signals from AGE A;Reference number: Z22355; MUID:98382502; PMID:9716402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.(Cross-references: UNIPROT:077145; UNIPARC:UPI000007ABA0; EMBL:AF072381; NID:g3694832; I C;Genetics: A.Gene: akt-2
A.Gene: akt-2
A.Fenction: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A;Penctiption: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine A;Penthway: signal transduction pathways regulating metabolism, development, and longevity C;Ruperfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology, protein P;111-113/Domain: pleckstrin repeat homology <PLK>F;11-113/Domain: protein kinase homology <RLK>F;11-113/Domain: protein kinase APP-binding motif F;209/Active site: Lys #status predicted F;337/Binding site: phosphate (Thr) (covalent) #status predicted
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                                                                                                                                                                   62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLH
                                                                                                                                                                                                                                                                                  122 SGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDY
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62;
  39; Mismatches
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Perfect score:

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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 1303057 seqs, 888780828 residues Searched:

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seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Patents NA:\* Issued Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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7         257.2         26.3         2311         3         US-09-016-473         Sequence           8         255.8         26.2         2396         3         US-09-949-1016-1735         Sequence           9         246.4         25.2         3321         3         US-09-225-749-24         Sequence           1         239.4         24.5         2245         3         US-09-225-749-24         Sequence           2         238.4         24.5         2274         3         US-09-772-647-3         Sequence           3         238.6         24.4         53.2         3         US-109-772-647-3         Sequence           4         23.5         24.4         53.2         3         US-109-772-647-3         Sequence           4         23.5         24.4         53.2         3         US-09-772-647-3         Sequence           5         23.1         24.5         34.6         3         US-09-772-647-3         Sequence           5         23.3         23.8         25.5         3         US-09-447-588-265         Sequence           5         23.3         23.8         25.5         3         US-09-447-588-265         Sequence           23.2<	7 257.2 26.3 2311 3 US-09-016-434-772 Sequence 246.4 25.2 2396 3 US-09-949-016-1735 Sequence 246.4 25.2 2396 3 US-09-949-016-1735 Sequence 246.4 25.2 3321 3 US-09-225-749-24 Sequence 229.4 24.6 2245 3 US-09-225-749-24 Sequence 239.4 24.5 2274 3 US-09-772-647-3 Sequence 239.4 24.5 2274 3 US-09-772-647-3 Sequence 233.2 23.8 25.6 3 US-09-487-558B-265 Sequence 233.2 23.8 25.6 3 US-09-817-310-1 Sequence 233.2 23.8 25.6 3 US-09-817-310-1 Sequence 222.4 23.0 2127 3 US-09-094-714A-48 Sequence 222.4 23.0 2127 3 US-09-094-716A-48 Sequence 222.4 23.0 2127 3 US-09-770-767-13509 Sequence 222.4 22.7 2346 3 US-09-740-756-13509 Sequence 222.4 22.7 2346 3 US-09-440-756-13509 Sequence 222.4 22.7 2346 3 US-09-490-016-839 Sequence 213.6 21.8 2705 3 US-09-490-016-839 Sequence 213.6 21.8 2705 3 US-09-490-016-1959 Sequence 213.6 21.8 2705 3 US-09-490-016-1959 Sequence 213.6 21.8 2715 3 US-09-490-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-839 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.8 2715 3 US-09-342-322-3 Sequence 213.7 2754 3 US-09-3	56	257.2	26.3	2311	٣	US-09-541-228-6	ý
8         255.8         26.2         2396         3 US-09-049-016-1735         Sequence           9         246.4         25.2         3321         3 US-09-023-655-1361         Sequence           2         240.4         24.5         245.3         3 US-09-023-647-3         Sequence           2         239.4         24.5         2274         3 US-09-772-647-3         Sequence           2         239.4         24.5         2274         3 US-09-772-647-3         Sequence           3         23.8         25.6         3 US-09-770-76-14090         Sequence           5         233.2         24.0         3456         3 US-09-487-558B-265         Sequence           5         233.2         23.7         224.4         3 US-09-487-558B-265         Sequence           233.2         23.7         224.4         3 US-09-47-74A-4         Sequence           225.4         23.7         224.4         3 US-09-74-714A-4         Sequence           225.4         23.7         224.4         3 US-09-76-74A-1         Sequence           225.4         23.7         23.4         3 US-09-76-74A-1         Sequence           225.4         23.7         23.4         3 US-09-76-76-13509         Sequence<	8 255.8 26.2 2396 3 US-09-949-016-1735 Sequence 240.4 24.5 2321 3 US-09-023-655-1361 Sequence 240.4 24.6 25.2 3321 3 US-09-023-655-1361 Sequence 240.4 24.5 2274 3 US-09-023-647-3 Sequence 239.4 24.5 2274 3 US-09-772-647-3 Sequence 239.4 24.5 2274 3 US-09-772-647-3 Sequence 233.2 24.0 3456 3 US-09-270-76-14090 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 233.2 23.8 2556 3 US-09-487-558B-265 Sequence 232.2 24.0 3456 3 US-09-487-558B-265 Sequence 225.4 23.0 2127 3 US-09-047-7147-48 Sequence 225.4 23.0 2127 3 US-09-047-7147-9 Sequence 225.4 22.0 232 3 US-09-270-767-13509 Sequence 2214.8 22.0 2324 3 US-09-270-767-13509 Sequence 213.6 21.8 27.5 3 US-09-9417-197-7 Sequence 213.6 21.8 27.5 3 US-09-949-016-839 Sequence 213.6 21.8 27.5 3 US-09-949-016-839 Sequence 213.6 21.7 2754 3 US-09-949-016-839 Sequence 213.6 21.7 2754 3 US-09-949-016-839 Sequence 213.6 21.7 2754 3 US-09-9429-322-3	27	257.2	26.3	2311	m	US-09-016-434-772	772
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1 239.4 24.5 2274 3 US-09-772-647-3 Sequence 238.4 24.5 2274 3 US-09-270-767-14099 Sequence 238.6 24.4 3 US-09-270-767-14099 Sequence 235.2 24.0 3456 3 US-09-270-767-14099 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 233.2 23.8 23.5 1413 3 US-09-248-796A-4379 Sequence 222.4 23.0 2127 3 US-09-78-796A-4379 Sequence 222.4 22.7 2346 3 US-09-78-796A-6 Sequence 222.4 22.7 2346 3 US-09-78-9-78-6 Sequence 232.4 22.7 2346 3 US-09-78-9-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8	1 239.4 24.5 2274 3 US-09-772-647-3 Sequence 238.4 24.5 2274 3 US-09-772-647-3 Sequence 238.4 24.5 2274 3 US-09-270-767-14090 Sequence 238.2 24.0 3456 3 US-09-270-767-14090 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 222.8 23.5 1413 3 US-09-044-714A-48 Sequence 222.4 23.0 2127 3 US-09-044-714A-48 Sequence 222.4 23.0 2127 3 US-09-704-7143.9 Sequence 222.4 22.7 212.3 US-09-704-7147-13509 Sequence 222.4 22.7 222.4 3 US-09-719-772 Sequence 213.6 21.8 27.5 3 US-09-417-197-72 Sequence 213.6 21.8 27.5 3 US-09-49-016-839 Sequence 213.5 21.7 2754 3 US-09-949-016-839 Sequence 212. 21.7 2754 3 US-09-949-016-839 Sequence Sequence 212. 21.7 2754 3 US-09-92-32-3	30	240.4	24.6	2245	r	US-09-225-749-24	24,
2 239.4 24.5 2274 3 US-10-228-931-3 Sequence 3 238.6 24.4 532 3 US-09-270-776-14090 Sequence 235.2 24.0 4 552 3 US-09-407-58B-265 Sequence 233.2 23.8 2556 3 US-09-407-58B-265 Sequence 233.2 23.8 2556 3 US-09-407-24A-1 Sequence 225.8 23.5 1413 3 US-09-04-714A-48 Sequence 222.4 23.0 2124 3 US-09-04-714A-48 Sequence 222.4 23.0 2124 3 US-09-762-258-3 Sequence 222.4 22.7 3 US-09-762-258-3 Sequence 222.4 22.7 3 US-09-762-258-3 Sequence 222.4 22.7 3 US-09-762-258-3 Sequence 2214.8 22.5 2751 3 US-09-417-197-72 Sequence 2213.6 218 218 218 218 218 218 218 218 218 218	2 239.4 24.5 2274 3 US-10-228-931-3 Sequence 235.2 24.4 532 3 US-09-270-767-14090 Sequence 235.2 24.6 135.8 3 US-09-270-767-14090 Sequence 233.2 23.8 256 3 US-09-817-310-1 Sequence 233.2 23.8 256 3 US-09-817-310-1 Sequence 233.2 23.8 255 3 US-09-94-714A-48 Sequence 229.8 23.5 1413 3 US-09-248-796A-4379 Sequence 225.4 23.0 2127 3 US-09-770-767-13509 Sequence 225.4 23.0 2127 3 US-09-770-767-13509 Sequence 2214.8 22.0 2324 3 US-09-417-197-72 Sequence 213.6 21.8 2705 3 US-09-49-016-839 Sequence 213.6 21.8 2705 3 US-09-49-016-839 Sequence 213.6 21.8 2705 3 US-09-49-016-839 Sequence 213.6 21.7 2754 3 US-09-429-322-3 Sequence Sequence 213.6 21.7 2754 3 US-09-429-322-3 Sequence	31	239.4	24.5	2274	m	US-09-772-647-3	'n
3         238.6         24.4         532         3         US-09-270-767-14090         Sequence           4         235.2         24.0         3456         3         US-09-487-558B-265         Sequence           5         233.2         23.8         2556         3         US-09-617-310-1         Sequence           7         23.2         23.7         2244         3         US-09-617-310-1         Sequence           8         23.2         23.7         244         3         US-09-617-310-1         Sequence           8         229.8         23.5         1413         3         US-09-704-714A-48         Sequence           9         225.4         23.0         1413         3         US-09-70-76A-13509         Sequence           9         225.4         22.7         2346         3         US-09-76A-13509         Sequence           1         219.8         22.5         2751         3         US-09-76A-13509         Sequence           2         214.8         22.0         2324         3         US-09-76A-6         Sequence           2         21.8         27.0         3         US-09-949-016-839         Sequence           3         21.6 <td>3 238.6 24.4 532 3 US-09-270-767-14090 Sequence 233.2 24.0 3456 3 US-09-487-558B-265 Sequence 233.2 23.8 2556 3 US-09-487-558B-265 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 229.8 23.5 1413 3 US-09-094-714A-48 Sequence 229.8 23.5 1413 3 US-09-248-796A-4379 Sequence 225.4 23.0 2127 3 US-09-248-796A-4379 Sequence 222.4 22.7 2346 3 US-09-248-796A-379 Sequence 2214.8 22.0 2324 3 US-09-470-976B-6 Sequence 2313.6 21.8 2705 3 US-09-49-016-839 Sequence 213.6 21.8 2705 3 US-09-949-016-839 Sequence 213.6 21.8 2715 3 US-09-949-016-1959 Sequence 213.6 21.8 2715 3 US-09-949-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.7 2754 3 US-09-323-3</td> <td>32</td> <td>239.4</td> <td>24.5</td> <td>2274</td> <td>ო</td> <td>US-10-228-931-3</td> <td>'n</td>	3 238.6 24.4 532 3 US-09-270-767-14090 Sequence 233.2 24.0 3456 3 US-09-487-558B-265 Sequence 233.2 23.8 2556 3 US-09-487-558B-265 Sequence 233.2 23.8 2556 3 US-09-817-310-1 Sequence 229.8 23.5 1413 3 US-09-094-714A-48 Sequence 229.8 23.5 1413 3 US-09-248-796A-4379 Sequence 225.4 23.0 2127 3 US-09-248-796A-4379 Sequence 222.4 22.7 2346 3 US-09-248-796A-379 Sequence 2214.8 22.0 2324 3 US-09-470-976B-6 Sequence 2313.6 21.8 2705 3 US-09-49-016-839 Sequence 213.6 21.8 2705 3 US-09-949-016-839 Sequence 213.6 21.8 2715 3 US-09-949-016-1959 Sequence 213.6 21.8 2715 3 US-09-949-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.8 2715 3 US-09-349-016-1959 Sequence 213.6 21.7 2754 3 US-09-323-3	32	239.4	24.5	2274	ო	US-10-228-931-3	'n
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7         232         23.7         2244         3 US-09-094-714A-48         Sequence           8         229.8         23.5         1413         3 US-09-248-4379         Sequence           9         225.4         23.0         10-09-770-76-76-13509         Sequence           0         222.4         22.7         2346         3 US-09-762-258-3         Sequence           1         219.8         22.5         2751         3 US-09-147-197-72         Sequence           2         214.8         22.0         2324         3 US-09-190-196-6         Sequence           2         214.8         2705         3 US-09-949-016-839         Sequence           3         213.6         21.8         2705         3 US-09-949-016-1959         Sequence	7 232 23.7 2244 3 US-09-094-714A-48 Sequence 229.8 23.5 1413 3 US-09-248-796A-4379 Sequence 222.4 23.0 2127 2146.9 US-09-248-796A-4379 Sequence 222.4 22.7 2146 3 US-09-762-258-3 Sequence 2214.8 22.5 2751 3 US-09-762-258-3 Sequence 2113.6 2118 22.5 2751 3 US-09-190-976B-6 Sequence 213.6 21.8 2775 3 US-09-949-016-1959 Sequence 213.6 21.8 2775 3 US-09-949-016-1959 Sequence 212 21.7 2754 3 US-09-949-016-1959 Sequence ALIGNMENTS	36	233.2	23.8	2556	m	US-10-355-724A-1	Sequence 1, Appli
8 229.8 23.5 1413 3 US-09-248-796A-4379 Sequence 4379, 225.4 23.0 2127 3 US-09-70-767-13509 Sequence 13505 Sequence 13505 Sequence 13505 Sequence 13505 Sequence 2, 227.4 22.7 2346 3 US-09-762-258-3 Sequence 7, 2751 3 US-09-417-197-72 Sequence 7, 2751 3 US-09-949-016-839 Sequence 7, 2751 3 US-09-949-016-839 Sequence 1959, 213.6 21.8 2705 3 US-09-949-016-1959	8 229.8 23.5 1413 3 US-09-248-796A-4379 Sequence 4379, 225.4 23.0 2127 3 US-09-0.767-13509 Sequence 13505 Sequence 13.0 Sequence 6.0 Sequence 6	37	232	23.7	2244	ო	US-09-094-714A-48	Sequence 48, Appl
9 225.4 23.0 2127 3 US-09-270-767-13509 Sequence 13505 US-22.4 22.7 2346 3 US-09-762-258-3 Sequence 3, Ag 1 US-09-762-258-3 Sequence 3, Ag 2 13.8 22.5 2351 3 US-09-317-197-72 Sequence 72, PS 2 13.8 22.0 2324 3 US-09-190-9768-6 Sequence 6, Ag 2 13.6 21.8 2705 3 US-09-949-016-839 Sequence 839, Ag 213.6 21.8 2715 3 US-09-949-016-1959	9 225.4 23.0 2127 3 US-09-270-767-13509 Sequence 13505 0 222.4 22.7 2346 3 US-09-762-258-3 Sequence 3. At 1 219.8 22.5 2751 3 US-09-417-197-72 Sequence 72, At 2 214.8 22.0 2324 3 US-09-417-197-72 Sequence 6, At 3 213.6 21.8 2705 3 US-09-99-016-839 Sequence 6, At 4 213.6 21.8 2715 3 US-09-949-016-839 Sequence 1959 5 212 21.7 2754 3 US-09-429-322-3 Sequence 3, At ALIGNMENTS	38	229.8	23.5	1413	m	US-09-248-796A-4379	437
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tive 0; Mismatches 0; Indels
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APPLICANT. Jefferson, Anne Brittlen Jefferson, Anne Brittlen Jefferson, Anne Brittlen Jefferson, Anne Brittle Brittlen Jefferson, Anne Brittle Brittlen Jefferson Je
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Best Local Similarity 100.
Matches 978; Conservative
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; ORGANISM: Homo sapiens
US-09-851-670-1
-09-851-670-1
Sequence 4, Application
Patent No. 6809194
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Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0	OY 1 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGAAACTACTAGGT 60	Db 531 TCTACAACCCATCATAAAGAAAGACAATGAATGATTTGACTATTTGAAACTACTAGGT 590 Oy 61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGGCAAGTGGAAATACTATGTTTTGA		Oy 121 ATGAAGATTCTGAAGAAGTGAAGGATGGAAGGATGAAGGGCACACACTTAACT 180	651	GARAGGAGAGTATTARAGGAGAGAGAGAGAGAGAGATTTTTTTT	OY 241 CAGACAAAAGACCGTTTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC 300	301 CALTITICTCGAGGGGGGGGTGTTTTCTGGAGCGGGGGGGGGG	Db 831 CATTTGTCGAGAGGCGCGGTGTTCTCTGAGGACCGCACGCTTTCTATGGTGCAGAAATT 890	891 GTCTGGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCCAAGTTGGAG	Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTTGCAAAGAA 480	Db 951 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTGGACTTTGCAAAGAA 1010 Ov 481 GGGATCACAGATGCCACCACCATGAAGAACATTCTGTGGCACTTCCAGAATATCTGGCACCA 540	1011 GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA	Oy 541 GAGGTGTTAGAAGATAATGACTAGTGGCCGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC 600	601 ATGTATGAAATGATGTGGGGAGGTTACCTTTCTACAACCAGGACCATGAGAAACTTTTT	DD 1131 ATGTATGAAATGATGTGGGAAGGTTACCTTTCTACAACCAGGACCATGAGAAATTTT 1190  Qy 661 GAATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTTCAGATGCAAAATCA 720  Db 1191 GAATTAATAATAGAAAATGATTAAATTTACTCCTCGAACACTCTCTTCAGATGCAAAATCA 1250	721 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT		Qy         781 GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840	841 AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT	Db 1371 AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT 143	901 GAIGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATAIGA 953	Db 1431 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATGTCA 1483	RESULT 3 US-09-771-161A-66 ; Sequence 66, Application US/09771161A	; Patent No. 6936450 ; GENERAL INFORMATION: ; APPLICANT: LEVINE, et al.
Oy 361 GTCTCTGCCTTGGACTATCTGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420	Db 776 Greterecetresaeraretaearrecesaaasarresaretaeerearereaasaretesas 835	Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTGGACTTTGCAAAGAA 480	54	968	Oy         541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTTGTC         600           Db         956 GAGGTGTTAGAAGATAATGACTAATGGCCGAGGAGTAGAGTGGTGGGGGTTGTGTGTG	601 AIGTAIGAAATGAIGACIAAGATAACCTITCTACAACCAGGACCAIGAGAAACTITIT	Db 1016 ATGTATGAAATGATGTGTGGGAGGTTACCTTTCTACAACGAGGACCATGAGAAACTTTTT 1075 OV 661 GAATTAATATTAATGGAAGACATTAAATTTCTTCTACAAAACTTTTTT 1075	1076 GAATTAATTAATGGAAGACAITAAATTTCCTCGAACACTCTCTTCAGAIGCAAAATCA	Oy 721 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT 780	781 GCAAAGAAATTATGAGAGACACCACTATGATGATAA 1840	Db 1196 GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1255	QY         84.1 ABAAAGCTIGTTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT         900           Db         1256 AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGTTACTTTTTTTT		Db 1316 GATGAAGAATTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT 1375 Ov 961 GGTATGGATGGATGGAC 978		RESULT 2 US-09-526-043-1 S. Sequence 1, Application US/09526043 Parent No. 6881555	GENERAL INFORMATION: ; APPLICANT: Guo, Kun	<pre>// APPLICANT: Pagnoni, Marco // APPLICANT: Clark, Kenneth // APPLICANT: Tvashchanko // APPL</pre>	; TITLE OF INVENTION: TOTAL ; FILE REPRENCE: A2278A-US ; CURRENT APPLICATION NUMBER: US/09/526.043	CURRENT FILING DATE: 2000-03-14; EARLIER APPLICATION NUMBER: 60/125,108	; EARLIER FILING DATE: 1999-03-19 ; NUMBER OF EGO ID NOS: 17	SCRIMARE: FACERLIR VEL. Z SEQ ID NO 1 LENGTH: 1570	TYPE: DN ORGANISM	9-0	Query Match 97.1%; Score 949.8; DB 3; Length 1570; Best Local Similarity 99.8%: Pred No. 1.2e.559;

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Pred. No. 7.5e-139;
0; Mismatches 245; Indels
; Sequence 5, Application US/09590740; Patent No. 6689807; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: St. Elizabeth's Medical Center; TITLE OF INVENTION: HMG COA Reductase Inhibitors for TITLE OF INVENTION: HMG COA Reductase Inhibitors for TITLE OF INVENTION: HMG COA REDUCTANGENIES; FILE REFERENCE: 49,784 (1417); CURRENT APPLICATION NUMBER: US/09/590,740; CURRENT FILING DATE: 2000-06-08; NUMBER OF SEQ ID NOS: 6; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.7%;
Best Local Similarity 73.4%;
Matches 685; Conservative 0
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                  CURRENT APPLICATION NUMBER: US/09/71,161A
CURRENT APPLICATION NUMBER: US/09/71,161A
CURRENT FILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: 09/724,676
FRIOR APPLICATION NUMBER: 136776
FRIOR FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: 135619
FRIOR FILING DATE: 2000-06-15
FRIOR APPLICATION NUMBER: 135619
FRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SEQ ID NO 66
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COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 07-Oct-1998
CLASSIFICATION: <university control of the control of the
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STREET: Suite 1800, Two Penn Center Plaza
CITY: Philadelphia
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Patent No. 6365151
GENERAL INFORMATION:
APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S.
England, James M.
TITLE OF INVENTION: CANCER VACCINE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
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APPLICATION UNMERS: PCT/US97/00582
FILING DATE: «UNKNOWN.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
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STRANDEDNESS: single
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APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
FILE REPERENCE: TTG-.035
CURRENT APPLICATION NUMBER: US/09/256,465
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 47
LENGTH: 1599
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Patent No. 6043090
GENERAL INFORMATION:
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Matches 673; Conservative
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ORGANISM: Homo sapiens
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                                                                                      Length 1599
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                                                                              Score 515.8; DB 3;
Pred. No. 2.5e-136;
0; Mismatches 262;
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                 52.7%;
72.0%;
                                                                              Query Match
Best Local Similarity 72.0°
Matches 673; Conservative
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US-09-167-322-3
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RESULT

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 52.7%; Score 515.8; DB 3; 72.0%; Pred. No. 2.5e-136; GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 PORTER DRIVE REFERENCE DOCKET NUMBER: PA-0001 US TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1004: SEQUENCE CHARACTERISTICS: US/09/023,655 Sequence 1004, Application US/09023655 Patent No. 6607879 ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071 LENGTH: 1599 base pairs CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH Best Local Similarity 72.0 Matches 673; Conservative PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: nucleic acid CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA INMEDIATE SOURCE: ; LIBRARY: GENBANK ; CLONE: 9178325 US-09-023-655-1004 FILING DATE: HI CLASSIFICATION: STRANDEDNESS: 94304 8 us-10-601-311-2.rni

	CTACATTCCGGAAAGATTGTGTACCTGAAGTATCTAATGCTGGAGAAA 438	GATGGCCACATAAAAATTACAGATTTGGAACTAAAGAGAAGAAGAGATGCAGCC 498	ACCATGAAGACATTCTGTGGCACCCAGAATATCTGGCACCAGAGGTGTTAGAAGATAAT 558  QY 204 TAGACATCCCTTTTTAACATACCTTCCTCAGAACACTTTTGTCTTCCAGAACACCCTTGTGTTT 263	GACTATGGCCGAGCAGTAGAGGCTTGTCATGTATGAAATGATGTGT         618         Qy         264         TGTGATGGCAGGCGAGCTGTTTTTCCATTTGTCGAGAGAGCGGGTGTT         323	GGGAGGCTTACCTTCTACAACCAGGAACCATGAGAACTTTTGAATTATATATA	GACATTABATTICCTCGAACACTCTTCAGATGCAAAATCATTGCTTTCAGGCTCTTG         738         384         TICCGGAAAGATTGTGTACCGTGATCCAAGTTGGAGAAAATCTTAGGCGAAAAGA         410	ATTARAGGATCCARATARAGGACCAGGACCAGGACCAGGACCACAGGACCACAGGACCACACAGAAGGACCACACCAC	CACAGITICITCTGGAGAGAAGATGTAAAAAGCTTGTACCACCT         SS         SO         CATGAAGACATTCTGGGACATCGAGAATATGATAAAAAGTTGTACCACAAAAAAAGTTGTACAAAAAAAA	TITADA OCTICA AGTA ACTICA AGATACTICA AGATA TITICA AGATA GATA AGATA AGA	CAGACTATTACAATAACATTTITGAAAAATTAATATTAATATTAATATTATAAGAAGA         621 GAGGTTACCTTTCTACAACCAGGACCATGAGAAACTTTITGAATTAATATTAATATTAAGAAGA         680	1995 GATCCCTTCCTCAAACCATTCTTCCCAAACCATTCTTCCCAAACCATTCTTC
 	Qy 379 CTACATTCCGG               Db 883 TTGCACTCGCG	Qy 439 GATGGCCACAT 	Oy 499 ACCATGAAGAC 	Qy 559 GACTATGGCCG 	Oy 619 GGGAGGTTACC	Qy 679 GACATTAAATT	Qy 739 ATAAAGGATCC 	Qy 799 CACAGTITCIT           Db 1303 CACAGGITCIT	Oy 859 TTTAAACCTCA 	Qy 919 CAGACTATTAC              Db 1423 CAGTCCATCAC	RESULT 8 Sequence 70, Application US/094 Sequence 70, Application US/094 Patent No. 6518021 GENERAL INFORMATION: APPLICANT: 01e THASTRUP, et al. TITLE OF INVENTION: A Method F. TITLE OF INVENTION: On A Cell FILE REFERENCE: 3759-0110P CURRENT APPLICATION NUMBER: US. CURRENT FILING DATE: 1999-10- SEQ ID NO 70 LENGTH: 2181 TYPE: DATE: 1999-10- SEQ ID NO 70 LENGTH: 2181 TYPE: DATE: 1899-10- FEATURE: COTHER INFORMATION: PKB-GGFP F FEATURE: COTHER INFORMATION: 75.5%; Best Local Similarity 72.5%; Best Local Similarity 72.5%;

us-10-601-311-2.rni

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                                      861 TAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGAAGAATTTACAGCTCA
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Pred. No. 9.2e-135;
0; Mismatches 254;
                                                                                                                    2076 GATGATCACCATCACACCACCTGACCAAGATGA 2108
                                                                                                     GACTATTACAATAACACCACCTGAAAAATATGA 953
                                                                                                                                                                                                                                                               APPLICANT: Brett P. Monia
APPLICANT: Brett P. Monia
APPLICANT: Lax M. Cowsert
TILE OF INVENTION: ANTISENSE MODULATION OF AK
FILE REFERENCE: RTS-0034
CURRENT APPLICATION NUMBER: US/09/212,771
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 47
LENGTH: 2610
                                                                                                                                                                                                                 ' Sequence 1, Application US/09212771
' Patent No. 5958773
' GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%;
72.5%;
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676; Conservative
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; LOCATION: (199)...(1641)
US-09-212-771-1
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                   RESULT 10
US-09-212-771-1
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Best Local S:
Matches 676
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                                                                                                                                                                                                                                                 Score 510.6; DB 3;
Pred. No. 8.5e-135;
0; Mismatches 254;
CURRENT APPLICATION NUMBER: US/09/417,197
CURRENT FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 138
                                                                                                                                                 OTHER INFORMATION: EGFP-PKB fusion
                                                                                                                                                                                                                                                Query Match 52.2%;
Best Local Similarity 72.5%;
Matches 676; Conservative
                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138
                                                                                    LENGTH: 2184
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
                                                                             TGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAAGGGATCACAGATGCAGCCAC
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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ADDRESSEE: INCYTE PF
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US-09-023-655-1206
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APPLICANT: Frech, Matchias
TITLE OF INVENTION: Screening Method
FILE REFERENCE: 4-20683/A/20684/PCT
CURRENT APPLICATION NUMBER: US/09/091,058
CURRENT FILING DATE: 1998-06-10
EARLIER PELLOGATION NUMBER: PCT/EP96/04814
EARLIER PELLING DATE: 1996-11-05
EARLIER APPLICATION NUMBER: 9225703.6
EARLIER PILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
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Patent No. 6054285
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; LOCATION: (199)..(1641)
US-09-091-058-1
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ORGANISM: Homo sapiens
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LENGTH: 2610
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Pred. No. 9.2e-135;
0; Mismatches 254;
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APPLICANT: St. Elizabeth's Medical Center
APPLICANT: St. Elizabeth's Medical Center
TITLE OF INVENTION: HMG COA REGuctase Inhibitors
FITLE OF INVENTION: Promoting Angiogenesis
FILE REFERENCE: 49,784 (1417)
CURRENT APPLICATION NUMBER: US/09/590,740
NUMBER OF SEQ ID NOS: 6
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ilarity 72.5%;
Conservative (
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CORGANISM: Homo sapiens
US-09-590-740-1
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SEQ ID NO 1
LENGTH: 2610
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                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-055
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1206:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                             HEREWITH
                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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| IMMEDIATE SOURCE:
| LIBRARY: GENBANK
| CLONE: 9190827
| US-09-023-655-1206
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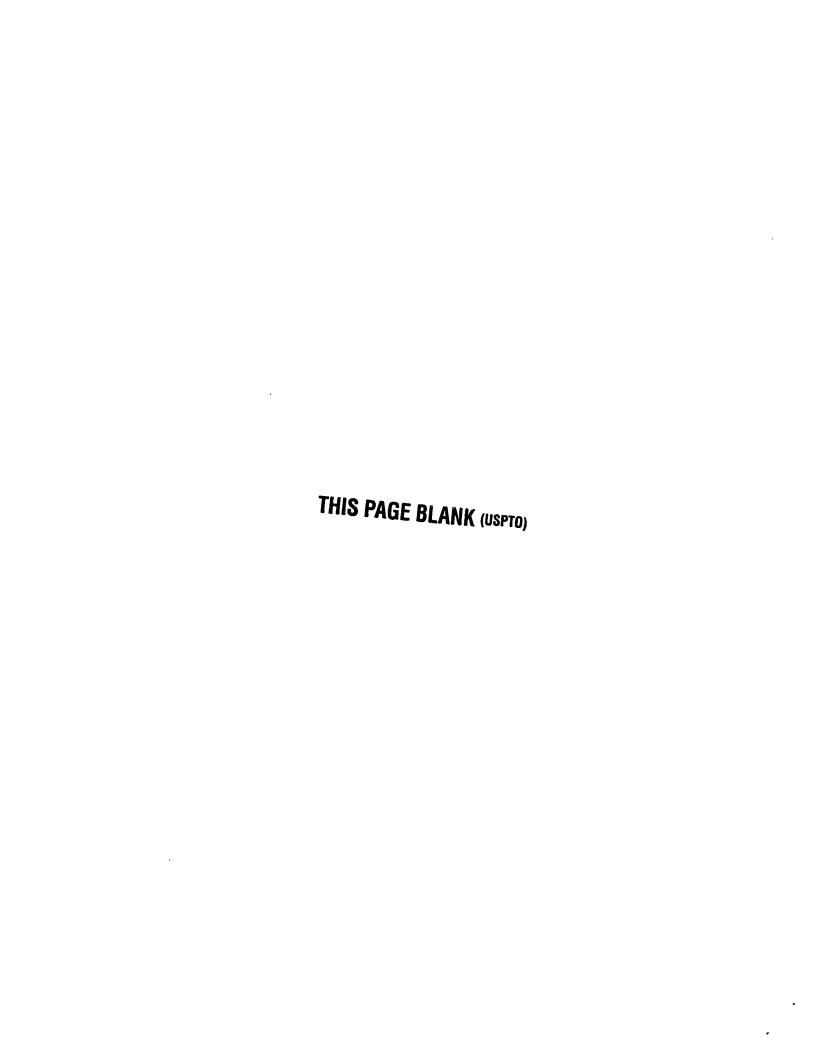
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                              426 CAGGCACCCCTTCCTCACTCGCCTGAAGTACTCTTTCCAGACCCACGACCGCCTCTGCTT
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APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3
CURRENT APPLICATION NUMBER: US/09/474,922A
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 89
LENGTH: 387
TUBERT TITLE OF TOWN OF AKT-3
LENGTH: 387
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, ORGANISM: Homo sapiens
US-09-474-922A-2
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TGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAAGGGATCACAGATGCAGCCAC
                               1053 cedechártraagarcacagacrircegecrereceaagagagagagarcaagacegreceac
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                                                                     CATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCAGAGGTGTTAGAAGATAATGA
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Fatent No. 6689807
GENERAL INFORMATION:
APPLICANT: Kenneth Walsh
TITLE OF INVENTION: HMG COA Reductase Inhibitors for TITLE OF INVENTION: Promoting Angiogenesis FILE REFERENCE: 49,744 (1417)
CURRENT PELLICATION NUMBER: US/09/590,740
CURRENT FILING DATE: 2000-06-08
NUMBER OF SEQ. ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.4%; Score 493; DB 3; L
llarity 72.0%; Pred. No. 6.7e-130;
Conservative 0; Mismatches 255;
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US-09-590-740-3
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Best Local Similarity
Matches 672; Conserv
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                                                                                                                     CTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTGATGAAGAATTTACAG 916
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Query Match 39.2%; Score 383.8; DB 3; Length 387; Best Local Similarity 99.5%; Pred. No. 4.3e-99; Matches 385; Conservative 0; Mismatches 2; Indels 0;
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Search completed: February 15, 2006, 05:41:40 Job time : 200 secs



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2006, 06:06:54; Search time 259 Seconds (without alignments) 3455.275 Million cell updates/sec
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1 tctacaacccatcataaaag.....atggtatggactgcatggac 978
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(cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6247088 seqs, 457523669 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                  US-10-601-311-2
                                                                                                                                                                           February 15,
                            Copyright
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IES	Description	-585-45 Sequence 45, Appl	26	US-11-170-693-66 Sequence 66, Appl		US-11-136-527-1823 Sequence 1823, Ap	-249-56 Sequence 56, Appl	US-11-136-527-7052 Seguence 7052, Ap		S	US-11-136-527-2486 Sequence 2486, Ap					US-10-955-054A-34 Sequence 34, Appl	6-527-3329 Sequence 3329, Ap		US-11-000-688-1538 Seguence 1538, Ap	US-11-136-527-3715 Sequence 3715, Ap	-561-339 Sequence 339, App	E61-220
SUMMARIES	ΩĪ	US-10-826-585-45	US-11-13	US-11-17	US-11-13	US-11-13	US-10-947-249-56	US-11-13	US-11-13	US-10-821	US-11-13	US-11-00	US-11-13	US-11-15	US-11-13	US-10-955	US-11-13	US-11-117-013-3	US-11-00	US-11-13	US-10-995-561-339	110 1 0 0 C C 1 3 3 0
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de	Query	100.0	88.1	53.7	52.9	52.8	52.7	41.1	27.6	26.5	25.9	25.2	24.2	23.5	23.5	23.1	22.8	22.7	22.7	22.4	22.2	22
	Score	978	861.4	525	517	516.2	515.8	401.8	269.6	258.8	253.6	246.4	236.4	229.8	229.4	226.4	223	222.4	222.4	219	216.8	0 710
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Sequence 2369, Ap	_	4035,	5919,	H	3,	Sequence 37, Appl	15,	32,	8	491, 7	532,	532,	1805,	270,	2671,	2887,	1709,	5351,	1709,	5351,	6045,		Sequence 1021, Ap
. US-11-136-527-2369	US-11		-		. US-11-091-883-344	US-10-770-726-37				US-11	us-	ns-	ns-		. US-11-136-527-2671	US-11-136-527-2887	. US-11-128-061-1709	. US-11-128-061-5351	US-11	US-11		US-11-128-061-1021	US-11-128-049-1021
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22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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gequence 45, Application US/10826585

| Reduction No. US20060008807A1
| GENERAL INFORMATION:
| APPLICANT: Immunivest Corporation
| APPLICANT: Equit. Brad
| APPLICANT: Poult. Brad
| APPLICANT: Waltiparameter analysis of comprehensive nucleic acids and
| TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and
| TITLE OF INVENTION: Morphological features on the same sample
| TITLE OF INVENTION: morphological features on the same sample
| TITLE OF INVENTION: morphological features on the same sample
| TITLE OF INVENTION: morphological features on the same sample
| TITLE OF INVENTION: morphological features on the same sample
| TITLE OF INVENTION: morphological features on the same sample
| FILE REFERENCE: IMMC 143 PCT/US 026, 585
| CURRENT FILING DATE: 2002-04-04
| PRIOR PAPLICATION NUMBER: 60/330669
| PRIOR PAPLICATION NUMBER: PCT/US 02/26867
| PRIOR FILING DATE: 2002-08-23
| NUMBER OF SEQ ID NOS: 131
| SOFTWARE: PatentIn version 3.3
| SEQ ID NO 45
| LENTH: APPLICATION NUMBER: MORE NOT NUMBER: MORE NOT NUMBER: MORE NOT NUMBER: MORE NOT NUMBER: MORE NUMBER: MORE
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Best Local Similarity 100.0
Matches 978; Conservative
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; ORGANISM: Human
US-10-826-585-45
US-10-826-585-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGGCCCTTGGTGGAGGGCCAGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAGATTCTGAAGAAAGAAGCATTATCGCAAAGGATGAAGTGGCACATACTCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
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                                                                                                                                           Gaps
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                                                                                                                                           56; Indels
                                                                                           Score 861.4; DB 11;
Pred. No. 4.5e-228;
0; Mismatches 56;
                                                                                             Query Match
Best Local Similarity 94.1%;
Matches 895; Conservative
                            norvegicus
; TYPE: DNA
; ORGANISM: Rattus
US-11-136-527-2956
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860

920

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1035 CCGCCTGCCCTTCTACAACCAGGACCACGAGAAGCTGTTCGAGCTGATCCTCATGGAGGA 1094
                                                                                .095 gárccgerreckadadadatregaecerraagaekenaarekerrekerekerekereka 1154
                                                                                                                                                                       1155 GAAGGACCCTACACAGAGGCTCGGTGGGGCTCTGAGGATGCCAAGGAGATCATGCAGCA 1214
                                                                                                                                                                                                                                                            CATTAAATTTCCTCGAACACTCTTCAGATGCAAAATCATTGCTTTCAGGGCTCTTGAT 740
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; Sequence 2318, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
    APPLICANT: Wyeth
; APPLICANT: Wyeth
; TILE REFERENCE: 031896-041000 (AM101086)
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2338
LENGTH: 2349
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Pred. No. 6.8e-133;
9; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1335 GATGATCACCATCACGCCCTGATCAAGATGA 1367
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; ORGANISM: Rattus norvegicus
US-11-136-527-2338
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Best Local Si
Matches 667;
                                           681
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                                       Š
                             Sequence 66, Application US/11170693

Publication No. US20060014186A1

GENERAL INFORMATION:

APPLICANT: Hodge, Timothy A.

TITLE OF INVENTION: METHODS FOR CENOTYPE SCREENING OF A STRAIN DISPOSED ON AN ITILE OF INVENTION: METHODS FOR CENOTYPE SCREENING OF A STRAIN DISPOSED ON AN ITILE OF INVENTION: METHODS FOR CENOTYPE SCREENING OF A STRAIN DISPOSED ON AN ITILE OF INVENTION: METHODS FOR CENOTYPE SCREENING OF A STRAIN DISPOSED ON AN ITILE OF INVENTION WHERE: US/11/170,693

CURRENT APPLICATION NUMBER: 00/230,371

PRIOR PILING DATE: 2005-06-04

PRIOR FILING DATE: 2001-09-06

PRIOR FILING DATE: 2005-03-08

PRIOR PILING DATE: 2005-03-08

PRIOR PILING DATE: 2005-03-08

PRIOR FILING DATE: 2005-03-08

PRIOR FILING DATE: 2005-06-24

MUMBER OF SEQ ID NOS: 73

SEQ ID NO 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTGTCTCTGCCTTGGACTATCTACA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 TICCGGAAAGA---TIGIGIACCGTGAICTCAAGTIGGAGAAICTAAIGCTGGACAAAGA 440
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11larity 73.4%; Pred. No. 3.5e-135;
Conservative 0; Mismatches 245;
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; ORGANISM: Mus sp.
US-11-170-693-66
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                US-11-170-693-66
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Sequence 56, Application US/10347249

Publication No US20050287541A1

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: Miki OHIRA

APPLICANT: Takeshi GOTO

APPLICANT: Yakahiro HIRATA

APPLICANT: Yakahiro HIRATA

APPLICANT: Saichi YAMADA

TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Metho

TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma
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                        ACCATGAAAACCTTSTGTGGTACCCCGGAGTACTTGGCGCCCTGAGGTGCTAGAGGACAAT
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CTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGAATCTAATGCTGGACAAA
                                                                          GATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAAGGGGATCACAGATGCAGCC
                                                                                                GATGGCCACATCAAGATCACTGACTTTGGCTTGTSCAAAGAGGGCATCAGTGATGGGGCC
                                                                                                                                                    ACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCAGAGGTGTTAGAAGATAAT
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APPLICANT: Wyeth
APPLICANT: Wounts, William M
APLICANT: Mounts, William M
APLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of FILE REPRENCE: 01896-041000 (AM)01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1823, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
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Best Local Similarity 71.7*
Matches 669; Conservative
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1479 TTCAAACCTCAGGTCACGTCCGAGGTCGACACAAGGTACTTCGATGATGAATTTACCGCC 1538
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      TITAAACCICAAGIAACAICIGAGACAGATACIAGAIGAAGAAIITACAGCI
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APPLICANT: Wyeth
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat (
FILE REFERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-05
SEQ ID NOS: 362830
SSCFTWARE: PatentIn version 3.2
LENGTH: 600
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                                                                                      1539 CAGTCCATCACAATCACACCCCTGACCGCTATGA 1573
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92.9%; Pred. No. 2.7e-101;
ive 0; Mismatches 32;
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                                                                                                                                                                           Sequence 7052, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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GRNERAL INFORMATION:
APPLICANT: Wyeth
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; ORGANISM: Rattus norvegicus
US-11-136-527-7052
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Matches 421; Conservative
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Pred. No. 1.3e-132;
0; Mismatches 262;
FILE REFERENCE: 117007
CURRENT APPLICATION NUMBER: US/10/947,249
CURRENT FILING DATE: 2004-09-23
FINIOR APPLICATION NUMBER: US 60/505,614
PRIOR APPLICATION NUMBER: 2003-09-25
NUMBER OF SEQ ID NOS: 200
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 1715
                                                                                                                                                                                                              52.7%;
72.0%;
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Best Local Similarity 72.0
Matches 673; Conservative
                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-947-249-56
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Best Local Similarity 57.0%;
Matches 514; Conservative
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ORGANISM: Homo sapiens
US-10-821-234-306
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                                    Rat Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 269.6; DB 11; Length 3201;
Pred. No. 1.6e-64;
0; Mismatches 404; Indels 3;
                TITLE OF INVENTION: Probe Arrays For Expression Profiling of FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SCO ID NOS: 362830
SOFTWARE: Patentin Version 3.2
SEQ ID NO 4033
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Mounts, William M
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US-11-136-527-4033
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Best Local Similarity
Matches 525; Conserv
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2471 AGCATGCATTTTTCCGGTATATCGACTGGGAGAAACTCGAACGCAAGGAGATTCAGCCAC 2530
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                                                                                       CITITIAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGAAGAATTTACAG 916
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andamani, Susan
APPLICANT: Andamani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
RIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
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APPLICANT: BERTUCH, Francois
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APPLICANT: HOULGATTE, Remi
TILLE OF INVENTIONS (GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILE REFERENCE: 1423-R-03
CURRENT FILING DATE: 2004-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
PRIOR PILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1184
LENGTH: 3017
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593 AGACTACATTAATGGCGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCCTGGA 652
                                                                                                                             653 ACCCCGTGCTTCTACGCAGCTGAAAATAGCCAGTGCCTTGGGTTATCTGCACTCCCT
                                                                               330 GGACCGCACACGTTTCTATGGTGCAGAAATTGTCTGCCTTGGACTATCTACATTCCGG
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Pred. No. 4e-58;
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| LOCATION: (1)..(3017)

| OTHER INFORMATION: protein Kinase c, beta 1(PRKCB1)

US-11-000-688-1184
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; Publication No. US20050287544A1
; GENERAL INFORMATION:
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US-11-000-688-1184
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APPLICANT: Worth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Pred. No. 3.8e-60;
1; Mismatches 370; Indels 9;
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Sequence 2486, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
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Best Local Similarity 57.5%;
Matches 514; Conservative
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24.2%;
55.6%;
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; ORGANISM: Rattus norvegicus
US-11-136-527-2878
                                                                                                                                                                                                             Matches 497; Conservative
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                         GAAAGACAATGAATTTTGACTATTTGAAACTACTAGGTAAAGGCACTTTTGGGAAAG
                                                 GGATGAAACTGACCGATTTTAACTTCCTAATGGTGCTGGGGAAAGGCAGCTTTGGCAAGG
                                                                                                                        AAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGA
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Mismatches 406; Indels
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Sequence 2878, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION: APPLICANT: Wyeth

US-11-136-527-2878

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GCCAGAATAAAGGAGACAGGAGAGCTGTACGCTGTGAAGGTGCTGAAGAAGGACGTCATC 1201
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                                        For Expression
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Pred. No. 2.26
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Express;
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-66
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2878
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                                                                                                                                  2011 CTĆĆCŤTTGÅGGCĆGÁCAATGÅGGACGÁCČTATŤTGÅGTCCAŤCCŤCCATGÁCGÁĆGŤGC 2070
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                                                TACCTTTCTACAACCAGGACCATGAGAAACTTTTTGAATTAATATTAATGGAAGACATTA
                                                                                                                                                                                                                               686 AATTTCCTCGAACACTCTTCAGATGCAAAATCATTGCTTTCAGGGCTCTTGATAAAGG
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APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031895-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patent In version 3.2
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Pred. No. 2e-53;
1; Mismatches 392; Indels
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Best Local Similarity 55.1%;
Matches 493; Conservative
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; ORGANISM: Rattus norvegicus
US-11-136-527-1950
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US-11-136-527-1950
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LENGTH: 3075
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APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Petcr H.
TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
FILE REFERENCE: P27, 880-A USA
CURRENT APPLICATION NUMBER: USA/11/152,366
CURRENT FILING DATE: 2005-06-14
FRIOR APPLICATION NUMBER: 60/579,307
FRIOR APPLICATION NUMBER: 60/579,307
FRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 295
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APPLICANT: PUSZTAL,
APPLICANT: SYMMANS, W. FRASER
APPLICANT: SYMMANS, W. FRASER
APPLICANT: AYERS, MARK
APPLICANT: AYERS, MARK
APPLICANT: STEC, JAMES
TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
FILE REFERENCE: UTXC:8800'S
CURRENT APPLICATION NUMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
NUMBER: OF SEQ ID NOS: 195
SOFTWARE: PLENTING DATE: 2.1
SEQ ID NO 34
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Matches 487; Conservative
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ORGANISM: Homo sapiens
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Sequence

Sequence 118, Applisequence 329, Applisequence 1206, Applisequence 1206, Applisequence 22, Applisequence 3, Applisequence 3134, Applisequence 9984, Applisequence 9984, Applisequence 9984, Applisequence 7, Applisequence 27402, Applisequence 27403, Applisequence 27, Appli

US-11-060-756-3130 US-11-060-756-3131 US-11-060-756-7402 US-11-060-756-7403 US-11-060-763-20291

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ALIGNMENTS

US-09-955-999-43 US-10-072-036-70 US-10-072-036-70 US-10-070-03-3 US-10-388-263-329 US-10-388-263-329 US-10-713-678-1 US-10-755-461-22 US-10-755-461-22 US-10-956-157-1382 US-10-956-157-4334 US-10-956-157-4334 US-10-198-846-9984 US-10-131-678-3 US-10-131-678-3 US-10-771-43-25901 US-11-097-143-25901 US-11-097-143-25901 US-11-097-143-25901 US-11-097-143-25901

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Sequence 4, Application US/10324985A

Publication No. US20030144204A1

GENERAL INFORMATION:
APPLICANT: Spencer, David
ITILE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REFERENCE: P02248US1/10106761
CURRENT APPLICATION NUMBER: US/10/324,985A
CURRENT FILING DATE: 2002-12-19
FRIOR APPLICATION NUMBER: US 60/342,155
FRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2811
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TYPE: DNA
ORGANISM: human
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US-10-324-985A-4
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1: /cgn2 6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*
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5: /cgn2 6/ptodata/1/pubpna/USO3B_PUBCOMB.seq:*
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7: /cgn2 6/ptodata/1/pubpna/USO3D_PUBCOMB.seq:*
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                         GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGGAAGGCAAGTGGAAAAATACTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
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PRIOR FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/445,216
PRIOR APPLICATION NUMBER: US 60/448,036
PRIOR APPLICATION NUMBER: US 60/448,036
PRIOR PILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-02-18
PRIOR PILING DATE: 2003-03-12
PRIOR PILING DATE: 2003-03-12
PRIOR PRICATION NUMBER: US 60/457,541
PRIOR PILING DATE: 2003-03-12
PRIOR PILING DATE: 2003-03-18
PRIOR PILING DATE: 2003-03-19
PRIOR PILING DATE: 2003-06-10
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Best Local Similarity 100.
Matches 978; Conservative
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
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US-10-753-267-107
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; Sequence 1, Application US/10394568; Squence 1, Application No. US20040002136A1; Squence 1, Application No. US20040002136A1; CANATION: APPLICANT: GUO, KUN

APPLICANT: IVASHCHENKO, YURI
APPLICANT: IVASHCHENKO, YURI
APPLICANT: IVASHCHENKO, YURI
APPLICANT: IVASHCHENKO, YURI
APPLICANT: OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT
FILE REFERENCE: A3399WO
CURRENT APPLICATION NUMBER: US/10/394,568
CURRENT FILING DATE: 2003-03-21
PRIOR PILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 1570
TYPE: DNA
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US-09-526-043-1
US-09-526-043-1
| US-09-526-043-1
| Sequence 1, Application US/09526043
| Publication No. US20030100049A1
| GENERAL INFORMATION:
| APPLICANT: Guo, Kun
| APPLICANT: Guo, Kun
| APPLICANT: Clark, Kennech
| APPLICANT: ICark, Kennech
| TITLE OF INVERTOR: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
| FILE REFERENCE: A3278A-US
| FILE REFERENCE: A3278A-US
| CURRENT APPLICATION NUMBER: 60/125,108
| EARLIER APPLICATION NUMBER: 60/125,108
| EARLIER FILING DATE: 1999-03-19
| NUMBER OF SEQ ID NOS: 119
                                                       .006 ATGTATGAAATGATGATGTGGGAGGTTACCTTTCTACAACCAGGACCATGAGAAACTTTTT
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; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1
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ORGANISM: Homo sapiens
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APPLICANT: Guo, Kun
APPLICANT: Guo, Kun
APPLICANT: Clark, Kenneth
APPLICANT: Clark, Kenneth
APPLICANT: Ivashchenko, Yuri
TILLE GINVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
FILE REPERENCE: A3278A-U8
CURRENT APPLICATION NUMBER: U8/11/063,691
CURRENT FILING DATE: 2005-02-23
PRIOR PILICATION NUMBER: U8/99/526,043
PRIOR PILICATION NUMBER: 60/125,108
PRIOR PLILING DATE: 1999-03-19
PRIOR PILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET: 2.1
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                                                                                 , Sequence 1, Application US/11063691
, Publication No. US20050142603A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-11-063-691-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                    97.1%; Score 949.8; DB 6;
99.8%; Pred. No. 2.3e-245;
tive 0; Mismatches 2;
                                                                                                                                         Best Local Similarity 99.8
Matches 951; Conservative
                   ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-10-394-568-1
ORGANISM: Homo sapiens
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APPLICANT: LEVINE, et al.

TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 136776

PRIOR APPLICATION NUMBER: 136776

PRIOR FILING DATE: 2000-06-11-28

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 273

SOFTWARE: Patentin version 3.0

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100.0%; Pred. No. 7.3e-175;
iive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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; TITLE OF INVENTION: Wethod to treat conditions associated; TITLE OF INVENTION: With insulin signalling dysregulation; FILE REFERENCE: 4-326.2
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 692
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99.8%; Pred. No. 2.4e-245;
tive 0; Mismatches 2;
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Matches 951; Conservative
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US-10-887-553A-692
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Publication No. US20030144204A1
GENERAL INFORMATION:
APPLICANT: Spencer, David
TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REPREBUCE: P02248031/10106761
CURRENT APPLICATION NUMBER: US10/324,985A
CURRENT FILING DATE: 2002-12-19
                                                                                                               891 TGCTTTGTGATGGAGTATGCCAACGGGGGTGAGCTGTTTTTCCACCTCTCTCGGGAGCGA
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Similarity 72.7%; Pred. No. 3.3e-131;
30; Conservative 0; Mismatches 255; Indels
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| Publication No. US20040126762A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: NOVEL Compositions and Methods in FILE REPRENCE: 52945200100
| CURRENT APPLICATION NUMBER: US/10/322,281
| CURRENT FILING DATE: 2002-12-17
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Mus musculus
US-10-322-281-412
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LENGTH: 1722
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ive 0; Mismatches 255; Indels
                                                                                                                                  Sequence 21, Application US/10735461

Publication No. US20050014264A1

GENERAL INFORMATION:

APPLICANT: ZHOU, Qionglin

APPLICANT: JANG, Zhen

TITLE OF INVENTION: METHOD OF INTRODUCING SIRNA INTO

TITLE OF INVENTION: ADIPOCYTES

CURRENT APPLICATION NUMBER: US/10/735,461

CURRENT APPLICATION NUMBER: 60/432427

PRIOR PILING DATE: 2003-12-11

PRIOR PILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 141

SOFTWARE: FASELSEQ for Windows Version 4.0
                                       919 CAGACTATTACAATAACACCACCTGAAAAATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 680; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Mus musculus
US-10-735-461-21
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                                                                                                                                                                          53.9%; Score 527; DB 6; Length 1772.7%; Pred. No. 3.3e-131; ive 0; Mismatches 255; Indels
PRIOR APPLICATION NUMBER: US 60/342,155
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                    Query Match
Best Local Similarity 72.7<sup>3</sup>
Matches 680, Conservative
                                                                                                      ; TYPE: DNA
; ORGANISM: mouse
US-10-324-985A-2
                                                                                     LENGTH: 1741
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TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REPREBLOE: P02248US1/10106/761
CURRENT APPLICATION WHERE: US/10/324,985A
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,155
PRIOR TILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                          1042 GATGGCCACATCAAGATCACTGACTTTTGGCTTGTGCAAAGAGGGCATCAGTGATGGAGCC
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                                                                                          379 CTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGAATCTAATGCTGGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      919 CAGACTATTACAATAACACCACCTGAAAAATATGA 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                   GACATTAAATTTCCTCGAACACTCTTCAGATGCAAAATCATTGCTTTCAGGGCTCTTG
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| Publication No. US20050048587A1
| GENERAL INFORMATION:
| APPLICANT: Rao, Patricia
| APPLICANT: Snyder, Jessica
| APPLICANT: Bagley, Andria
| TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
| TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
| TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
| FILE REFERENCE: TLN-025
| TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
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Pred. No. 4.4e-131;
0; Mismatches 255; Indels
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                                                                                                                                                                3;
                                                                                                                                    Length 1443;
                                                                                                                                 Score 525; DB 10; Length 1
Pred. No. 1e-130;
0; Mismatches 245; Indels
 PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 66
LENGTH: 1443
                                                                                                                                S3.7%;
Best Local Similarity 73.4%;
Matches 685; Conservative 0
                                                                       TYPE: DNA ORGANISM: Mus sp.
                                                                                                      US-11-166-990-66
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Fublication No. USZO050239125A1
GENERAL INFORMATION:
APPLICANT: Hodge, Timothy A.
TITLE OF INVENTION: METHODS FOR GENOTYPE SCRIFILE OF INVENTION: METHODS FOR GENOTYPE SCRIFICATION NUMBER: US/11/166,990
CURRENT APPLICATION NUMBER: GO/230,371
PRIOR APPLICATION NUMBER: GO/230,371
PRIOR APPLICATION NUMBER: 60/230,371
PRIOR APPLICATION NUMBER: 09/945,952
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US-11-166-990-66
; Sequence 66, ApI
; Publication No.
; GENERAL INFORMAT
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APPLICANT: St. Elizabeth's Medical Center
TITLE OF INVENTION: HGG CA Reductase Inhibitors for
TITLE OF INVENTION: Promoting Angiogenesis
FILE REFERENCE: 49,784 (1417)
CURRENT APPLICATION NUMBER: US/10/713,678
CURRENT APPLICATION NUMBER: US/09/590,740
PRIOR APPLICATION NUMBER: US/09/590,740
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: ESSEED for Windows Version 3.0
SEQ ID NO 5
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73.4%; Pred. No. 1.4e-130;
iive 0; Mismatches 245;
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; Publication No. US20040122077A1
; GENERAL INFORMATION:
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                                                                                                                                       Sequence 1, Application US/10324985A
Publication No. US20030144204A1
GENERAL INFORMATION:
APPLICANT: Spencer, David
TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REPERENCE: P02248US1/10106761
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,155
PRIOR APPLICATION NUMBER: US 60/342,155
SPIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 12
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Pred. No. 1.4e-130;
0; Mismatches 245; Indels
                        921 GACTATTACAATAACACCACCTGAAAAATATGA
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Best Local Similarity 73.4%;
Matches 685; Conservative 0
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TYPE: DNA
ORGANISM: mouse
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AAA62451 standard; cDNA; 1440 BP.
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaa62451 Human Akt	Abl50839 Human Akt	Aaa62450 Human Akt	Adn71939 Human ser	Adt99288 Human AKt	Aac61592 DNA encod	Adc26888 DNA encod	Adq88265 Human 141	Aac77341 Human ORF	Aaa96637 DNA encod	Aah79025 Human Akt	Aaa89264 Human ser	Adg85244 Human Chr	Adz49363 Insulin s	Adn71941 Chicken s	Abd33334 Murine ca	Adc26886 DNA encod	Adp48781 Mouse Akt	Adx01484 Human tol	
	3 ID	AAA62451	3 ABL50839	1 AAA62450	.2 ADN71939	.3 ADT99288	1 AAC61592	.0 ADC26888	.3 ADQ88265	3 AAC77341	1 AAA96637	4 AAH79025	I AAA89264	12 ADG85244	14 ADZ49363	12 ADN71941	13 ABD33334	10 ADC26886	12 ADP48781	L4 ADX01484	
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	8.66	97.1	97.1	97.1	97.1	97.1	61.8	53.9	53.9	53.9	53.9	
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Claim 4; Fig 1; 61pp; English.

especially cancer.

Adc26889 DNA encod	Aaa09078 Wild type	Aad28550 Mouse Akt	Adc26885 DNA encod	Adp48780 Mouse Akt	Adx01483 Human tol	Adl25356 ARK5 rela	Adq84311 Human tum		Adg83643 Human tum	Adq85783 Human tum	Acn40577 Tumour-as	Abd33336 Human can	Abl50838 Human Akt	Aat71252 Mouse Akt	Aaa08448 Human Akt	Aaz60814 Nucleotid	Adc26887 DNA encod	Adi31678 Human cDN	Adn71937 Human pro	Ads83745 Human lym	Abv94263 Breast ca	Adp48783 Human Akt		Acn43263 Human dia	Adx01463 Human tol
ADC26889	AAA09078	AAD28550	ADC26885	ADP48780	ADX01483	ADL25356	ADQ84311	ADQ86862	ADQ83643	ADQ85783	ACN40577	ABD33336	ABL50838	AAT71252	AAA08448	AAZ60814	ADC26887	ADI31678	ADN71937	ADS83745	ABV94263	ADP48783	AD226090	ACN43263	ADX01463
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53.7	53.7	53.7	53.7	53.7	53.7	53.7	52.9	52.9	52.9	52.9	52.9	52.9	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.4
525	525	525	525	525	525	525	517.4	517.4	517.4	517.4	517.4	517.4	515.8	515.8	515.8	515.8	515.8	515.8	515.8	515.8	515.8	515.8	515.8	515.8	512.2
20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

New human serine/threonine kinase protein and the polynucleotide encoding the protein, useful for preparing a medicament for treating disorders associated with human serine/threonine kinase protein activity, Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytostatic; apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE; chromosome 1q43-44; ss. Location/Qualifiers /\*tag= a /product= "Akt-3" 99WO-GB004311. 98GB-00028375. Masure SLJ, Richardson A; 1. .1440 /\*tag= a (JANC ) JANSSEN PHARM NV. WPI; 2000-498840/44. P-PSDB; AAB13393. WO200037613-A2 17-DEC-1999; 22-DEC-1998; 29-JUN-2000. Key  a

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The present sequence is the coding region of the nucleotide sequence that encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also known as protein kinase B (PKB) or "related to A and C protein kinase" (RAC-PK). The gene encoding Akt-3 is located on human chromosome 1, region q43-q44. A human hippocampal EST sequence that showed high similarity to the rat RAC-PKgamma sequence was used to design primers for 3 rapid amplification of cDNA ends (3 RACE). The sequence obtained in the first round of 3' RACE was used to design primers for a second round. The complete sequence was then amplified from human hippocampal cDNA by CR using primers based on the product of the second round of 3' RACE. Akt can inhibit apoptosis induced by detachment from the extracellular matrix. The Akt-3 nucleic acid molecule and protein may be used as matrix. The Akt-3 nucleic acid molecule and protein may be used as Akt-3 protein, and so stimulate apoptosis, may also be used to treat diseases associated with Akt-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, Hsp90 beta, Hsp90 alpha, Akt1, Akt2, Akt3, apoptosis regulation, apoptosis, serine/threonine kinase, heat shock protein; anticancer; cytostatic; cardiant, vasotropic, hepatocropic, neuroprotective, antidiabetic; nootropic, cancer; diabetes, Alzheimer's disease; cell death, radiation; brain ischaemia; cardiac ischaemia; gene; se.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulation of apoptosis by promoting or inhibiting the intracellular binding of Akt with Hsp90, useful for prevention and treatment of apoptosis-regulation associated diseases including cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Human Akt3 encoding cDNA SEQ ID NO:10.
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transformed cells; (7) screening compounds for their ability to modify intracellular Akt activity by contact with cells expressing Akt or Hsp90; and (8) drug compositions containing antibodies recognizing the binding domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and Hsp90 have cytostatic, cardant, vasotropic, hepatotropic, antidiabetic, neuroprotective and nootropic activities. Blockade of the binding of Hsp90 with Akt increases the sensitivity of cells to apoptosis induction. Akt and Hsp90 can be used in the prevention and treatment of diseases with which apoptosis regulation is associated, including cancer (such as gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and prostate cancer), diabetes, Alzheimer's disease, cell death caused by radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The present sequence encodes human Akt3 which is used in the exemplification
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Best Local Similarity 100.0%; Pred. No. 1.3e-257;
Matches 978; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also known as protein kinase B (PKB) or "related to A and C protein kinase" (RAC-PK). The gene encoding Akt-3 is located on human chromosome 1, region q49-q44. A human hippocampal BST sequence that showed high similarity to the rat RAC-PKgamma sequence was used to design primers for 3' rapid amplification of cDNA ends (3' RACB). The sequence bottained in the first round of 3' RACE was used to design primers for a second round. The complete sequence was then amplified from human hippocampal cDNA by PCR using primers based on the product of the second round of 3' RACE. Akt can inhibit apoptosis induced by detachment from
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                                                                                                                                                                                                                                                                                                                                                                                                           Human, Akt-3; protein kinase B; PKB; serine/threonine kinase; cytostatic;
apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
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 GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT
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the extracellular matrix. The Akt-3 nucleic acid molecule and protein may
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           be used as medicaments for treating cancer. Agents which influence the activity of Akt-3 protein, and so stimulate apoptosis, may also be used to treat diseases associated with Akt-3
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The present invention describes a composition (CI) which comprises a kinase pathway inhibitor (a) and an anti-prostate cancer compound (b). Also described: (l) identification of a mitogen-activated protein (MAP) kinase pathway inhibitor involving incubating an artivable MAP kinase pathway and selecting the molecules which inhibit the activation of the MAP kinase pathway, and (2) identification of a prostate cancer inhibitor. Involving incubating a cell with hydroxyflutamide and potential inhibitor, and assaying the level of activation of MAP kinase pathway or phosphatidylinositol 3-kinase (PISK)/Akt kinase pathway. Cl has cytostatic activity, and can be used as a MAP kinase pathway or phosphatidylinositol 3-kinase (PISK)/Akt kinase inhibitor.

Cytostatic activity, and can be used as a MAP kinase inhibitor, and androgen receptor (AR) inhibitor. Cl can be used in the treatment of prostate cancer; for identifying a MAP kinase pathway inhibitor; for identifying a prostate cancer inhibitor; and for reducing the number of prostate cancer cells in a sample. The composition Cl provides effective combination thereby as compared to prior therapies. The present sequence encodes
1316 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCCTGAAAAATATGATGAGGAT 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase pathway inhibitor; anti-prostate cancer;
mitogen-activated protein kinase pathway inhibitor;
MAP kinase pathway inhibitor; prostate cancer inhibitor;
phosphatidylinositol 3-kinase/Akt kinase pathway;
PI3K/Akt kinase pathway; cytostatic; MAP kinase inhibitor;
phosphatidylinositol 3-kinase/Akt kinase inhibitor;
PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
human; serine/threonine kinase Akt-3; chromosome 1; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human serine/threonine kinase Akt-3 encoding cDNA SEQ ID NO:25.
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                          Length 1547;
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                        100.0%; Score 978; DB 12;
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tive 0; Mismatches 0;
 BP; 515 A; 276 C; 348
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Akt3; AKt3 inhibitor; tumour; cancers; atherosclerosis; psoriasis; autoimmune diseases; bacterial infection; viral infection; HIV infection; hepatitis; antiarteriosclerotic; antibacterial; anti-HIV; antiinflammatory; antipsoriatic; cytostatic; hepatotropic; immunosuppressive; virucide; human; protein kinase B; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to an Akt3 inhibitor, where the inhibitor is an antisense molecule capable of inhibiting the expression of human Akt3. The Akt3 inhibitor is useful for preparing a medicament for modulating cell proliferation and for treating tumours, cancers, atherosclerosis, psoriasis, autoimmune diseases, bacterial infections arviral infections like human immunodeficiency virus 1 (HIV) infections wheparitis. The present sequence is the human Akt3 cDNA. Akt3 is also known as protein kinase B.
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The present sequence encodes a human protein kinase B gamma (PKB) polypeptide. PKB is activated by insulin or insulin growth factor 1. Lipid products of phosphoinositide 3-kinase act in insulin signalling by binding to pleckstrin homology domains of PKB. PKB polypeptides any be used as a source of probes and primers. PKB polypeptides are used to raise antibodies, which are used in diagnostic assays. The polypeptides are also useful for screening for compounds which affect insulin
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Novel human protein kinase B gamma polynucleotides and polypeptides useful as probe or primers in polymerase chain reaction and to raise antibodies useful in diagnostic assays for detecting polypeptide
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ligand-binding domain. The composition and methods are useful in modulating apoptosis or in treating myocardial infarction or hyperproliferative diseases such as ancer, rheumatoid arthritis, inflammatory bowel disease, osteoarthritis, leiomyomas, adenomas, lipomas, haemangiomas, fibromas, vascular occlusion, restenosis, lipomas, pre-neoplastic lesions (e.g. adenomatous hyperplasia or prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy leukoplakia or psoriasis. The present sequence represents DNA encoding
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100.0%; Pred. No. 1.7e-257;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel compound that is capable of treating carditovascular or thrombotic disorder. Specifically, it refers to the identification of nucleic acid molecules, and the encoded proteins thereof, which are differentially expressed in cardiovascular disease
                                                                                                                                                                                                                                                                                                                                        human; gene; ds; cardiovascular disorder; thrombotic disorder; differential expression; gene thorapy; aberrant vascularisation; atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia; dyslipidaemia; high blood pressure; heart failure; cardiant; thrombolytic; anticoagulant; antilipaemia; hypotensive; cardiant; rac gamma Ser/Thr protein kinase; RAC-PK-gamma.
                                                 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT
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                   1186 GCAAAAGAAATTATGAGACACAGTTTCTTCTGGAGTAAACTGGCAAGATGTATATGAT 1245
                                                                                                                                                                      1306 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppessant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidialamatory; antitiansemic; gene therapy; cancer; proliferative antithyroid; antiansemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bronne damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                           1246 AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTTTT
                                                                                                                                GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT
                                                          AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT
Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX ORF2896 polynucleotide sequence SEQ ID NO:5791.
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dermatological, immunosuppressive, antiniflammatory; antibacterial, antivital; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The mucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID) AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic annemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human Akt3 protein. Expression of Akt3 prevents apoptotic cell death induced by apoptotic stimulating kinase 1 (ASK1). The Akt3 polypeptide is useful for inhibiting cell death, preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or necrosis in a patient suffering from myocardial infarction or ischemia reperfusion injury. The polypeptide is also useful for treating myocardial infarction or ischemia reperfusion injury, where the reperfusion injury is myocardial ischemia reperfusion injury or is associated with stroke, liver damage, renal failure, organ transplantation or coronary artery by pass grafting
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GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel AKT3 nucleic acid and proteins capable of preventing death induced by apoptosis stimulating kinase 1 useful for myocardial infarction or ischemia reperfusion injury.
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                                                                                                                                                                                                                                                                 encoding a human Akt3 polypeptide.
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126. .1523
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Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

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97.1%; Score 949.8; DB 3;
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ive 0; Mismatches 2;
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Matches 951; Conservative
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encoding cDNA SEQ ID NO 1.

(first entry)

Location/Qualifiers 126. .1523 /\*tag= a /product= "Akt3"

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The invention relates to human Akt3 protein (AH/PH-domain containing serine/threonine kinase, Akt) comprising a fully defined sequence serine/threonine kinase, Akt) comprising a fully defined sequence (AAG78018) of 465 amino acids, its splice variant or allelic variant, where the encoding polynucleotide hybridises under stringent conditions with a nucleic acid containing a uncleotide sequence (AAH79025) of 1570 base pairs defined in the specification. Akt3 has cerebroprotective, corrective, corrective, and inhibitor of apoptosis and/or apoptosis and chaptotrophic activity, as an inhibitor of apoptosis and/or apoptosis of stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a cereplatory region is useful for inhibiting cell death in cardiac mycocytes cregulatory region is useful for inhibiting cell death in cardiac mycocytes regulatory region is useful for inhibiting cell death associated infarction or ischaemia reperfusion injury, particularly that associated with stroke, liver damage, renal failure, organ transplantation or coronary artery bypass grafting Agonist of Akt3 activity during treatment of patients suffering from mycoradial infarction or ischaemia reperfusion injury and inhibitors of Akt3 activity during treatment of patients suffering from mycoradial corrects cells from apoptosis. Gene therapy using Akt3 reduces the corrects cells from apoptosis. Gene therapy using Akt3 reduced to patients with existing heart failure, gene therapy with Akt3 retards the process of ventricular dilation and slows down disease progression. Akt3 death by anonyone is useful for treating other disease states, involving cell death by anonyone is successed the adverse second cell failure.
                                                                                                                                                        cerebroprotective; nootropic; neuroprotective; antiarthritic; osteopathic; vasotropic; hepatotrophic; inhibitor of apoptosis; ASK1; apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction; ischaemia reperfusion injury; stroke; organ transplantation; coronary artery bypass; tumour cell survival; gene therapy; Alzheimer's disease; osteoarthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding human Akt3 protein, useful for inhibiting or death and treating myocardial infarction, ischemia reperfusion injury associated with stroke, liver damage and renal failure.
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                                                                                                                                     Human; Akt3; AH/PH-domain containing serine/threonine
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Clark KL, Ivashchenko YD;

Pagnoni MF,

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            TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTTGACTATTTGAAACTACTAGGT
                                                                   ATGAAGATTCTGAAGAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACT
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Gaps

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Indels

7

0; Mismatches

Query Match
Best Local Similarity 99.8%;
Matches 951; Conservative

Score 949.8; DB 4; Length 1570; Pred. No. 7.5e-250;

240

540

900

890

950 480 720

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1011 GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA 1070
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                                      GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
                                                                                                          CAGACAAAAGACCGTTTGTGTTTTGTGAATGTTAATGTTAATGGGGGCGGAGCTGTTTTTC
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                    GAAAGCAGAGTATTAAAGGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
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126. .1523
/*tag= a
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AAB1996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase
capable of inducing vascular endothelial growth factor (VECF) expression.
The sequence was deduced from 2 cDNA clones isolated from a human heart
c DNA library using a human Akt3 partial clone as probb. Akt3 is shorter
c CDNA library using a human Akt2 (see AAB19998) and there is no
c significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of
the molecules. A claimed method of inducing expression of VEGF in a cell
involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding
involves administering Akt1, Akt2 or Akt3, or a patient suffering from an
ischaemic condition, especially creebrovascular, renal, pulmonary, limb
or myocardial ischaemia, or ischaemic, idiopathic or hypertrophic
c ardiomyopathy. The result is beneficial collateral blood vessel
cormation. A claimed method of inhibiting angiogenesis in a patient
c suffering from a tumour, comprises inhibiting the level of Akt activity
c n the patient, thereby inhibiting production of VEGF. The method
comprises introducing an Akt antisense uncleic acid, an intracellular
c binding protein (e.g. a scFV) that specifically binds the Akt protein, or
a nucleic acid encoding a dominant negative form of an Akt
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                                              Akt3; human; protein kinase; vascular endothelial growth factor; VEGF; inducer; ischaemia; cardiomyopathy; anglogenesis; tumour; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing expression of vascular endothelial growth factor, useful for treating an ischemia, condition, e.g. cerebrovascular ischemia, renal ischemia or pulmonary ischemia, comprises administering a serine/threonine protein kinase Akt protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACTATTTGAAACTACTAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;
                 Human serine/threonine protein kinase Akt3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 55-58; 67pp; English
                                                                                                                                              Location/Qualifiers
126. .1523
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                      (AVET ) AVENTIS PHARM PROD INC
                                                                                                                                                                                                                                                                                                                     99US-0138724P.
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P-PSDB; AAB19996.
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Best Local Similarity
Matches 951; Conserv
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03-NOV-1999;
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1431 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATGTCA 1483
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/product= "Chrysosporium associated protein"
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us-10-601-311-2.rng

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                                   GTCTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTGTACCGTGATCTCAAGTTGGAG
                                                                                                      AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1371 AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT
                    GTCTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG
                                                                                 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAA
                                                                                                                                                GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA
                                                                                                                                                                   .011 GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACA
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(MAJJ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a mutant Chrysosporium strain comprising a nucleic acid sequence encoding a polypeptide of interest. A mutant Chrysosporium strain is useful for producing a polypeptide of interest by culturing a mutant Chrysosporium strain under conditions permitting expression of the protein or polypeptide, and recovering the subsequently produced polypeptide of interest. The conditions further permit secretion of the protein or polypeptide of interest. The polypeptides are useful for hydrolysing beta-glucosidic bonds. A polypeptide is useful for hydrolysing beta-xylosidic bonds. The present sequence represents human Chrysosporium associated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Novel mutant Chrysosporium strain comprising nucleic acid sequence encoding polypeptide of interest such as proteases and lipases, the nucleic acid sequence being operably linked to expression-regulating
                                                                                                                                                                                                                                                                                                                              Parriche M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 949.8; DB 12; Length 1570;
Pred. No. 7.5e-250;
0; Mismatches 2; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            RP, Olson PT, Sinitsyn AP,
Punt PJ, Van Zeijl CMJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 1; 70pp; English.
                                                                                             06-OCT-1998; 98WO-EP006496.
06-OCT-1999; 99WO-NL000618.
13-APR-2000; 2000US-00548938.
                                                                21-MAR-2003; 2003US-00394568
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99.8%;
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Best Local Similarity 99.8'
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                                                                                                                                                            EMALFARB M A.
BURLINGAME R P.
OLSON P T.
                                                                                                                                                                                                          SINITSYN A P.
PARRICHE M.
BOUSSON J C.
PYNNONEN C M.
                                                                                                                                                                                                                                                                            PUNT P J.
VAN ZEIJL C M
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US2004002136-A1
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                                01-JAN-2004
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GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method for treating, preventing or ameliorating pathological conditions associated with dysregulation of the finalin signaling pathway (ISP). The method comprises administering to a subject a modulator for ISP-regulated proteins or a pharmaceutical composition comprising the described modulator. The method is useful for treating, preventing or ameliorating pathological conditions associated with dysregulation of the ISP such as Type II diabetes or Type A syndrome of insulin resistance. The present sequence is a human homolog of a brosophila gene regulated by ISP. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in sequence. Health from USPTO at sequence contained in sequence. Luspto.gov/sequence.html?DocID=20050085436.
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
with dysregulation of the insulin signaling pathway (ISP) comprises administering to a subject an amount of a modulator of any of the proteins regulated by ISP.
                                                                                                                                                                                                                                                                                                                                                                            Score 949.8; DB 14; Length 1703;
Pred. No. 7.7e-250;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                              Sequence 1703 BP; 576 A; 316 C; 387 G; 424 T; 0 U; 0 Other;
                                                                     Disclosure; SEQ ID NO 692; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.8%;
Matches 951; Conservative 0
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               The present invention describes a composition (C1) which comprises a kinase pathway inhibitor (a) and an anti-prostate cancer compound (b). Also described: (1) identification of a mitogen-activated protein (MAP) kinase pathway inhibitor involving incubating an antiandrogen or a library of molecules with a cell containing an activable MAP kinase pathway and selecting the molecules which inhibit the activation of the MAP kinase pathway; and (2) identification of a prostate cancer inhibitor involving incubating a cell with hydroxyflutamide and potential inhibitor, and assaying the level of activation of MAP kinase pathway or phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
                                                                840
                                                                                                                              900
                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase pathway inhibitor; anti-prostate cancer; mitogen-activated protein kinase pathway inhibitor; mitogen-activated protein kinase pathway inhibitor; phosphatidylinositol 3-kinase/Akt kinase pathway; plik/Akt kinase pathway; cytostatic; MAP kinase inhibitor; phosphatidylinositol 3-kinase/Akt kinase inhibitor; prostatic; Plik/Akt kinase inhibitor; prostatic chicken; serine/threonine protein kinase; akt1; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition useful in the treatment of e.g. prostate cancer comprises a kinase pathway inhibitor and an anti-prostate cancer compound.
                                                                                                                                                                                                                                                                                                                                                                                                        Chicken serine/threonine protein kinase (akt1) encoding cDNA SEQ ID:27
                                                                                                                                                GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT
                                                                                                                              AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "serine/threonine protein kinase (aktl)"
                                                                                                                                                                                            GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGA
                                                                                                                                                                                                               1387 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATGTCA
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466. .1908
                                                                                                                                                                                                                                                                                                          ADN71941 standard; cDNA; 2277
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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cytostatic activity, and can be used as a MAP kinase inhibitor, phosphatidylinositol 3-kinase (P13K)/Akt kinase inhibitor, and androgen receptor (AR) inhibitor. Cl can be used in the treatment of prostate cancer; for identifying a MAP kinase pathway inhibitor; for identifying a prostate cancer inhibitor; and for reducing the number of prostate cancer calls in a sample. The composition Cl provides effective combination therapy as compared to prior therapies. The present sequence encodes chicken serine/threonine protein kinase (aktl), which is used in the exemplification of the present invention.
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Sequence 2277 BP; 672 A; 490 C; 549 G; 566 T; 0 U; 0 Other;

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2 4211 DF; 012 A; 450 C; 349 G; 300 I; 0 U; 0 OLITEL;	'Match 61.8%; Score 604.2; DB 12; Length 2277; Local Similarity 77.9%; Pred. No. 5.6e-155; Loservative 0; Mismatches 208; Indels 3; Gaps	4 ACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACTATTTGAACTACTAGTAAA 	GGCACTTTTGGGAAAGTTATTTGGTTCGAGAAAGGCAAGTGGAAATACTATGCTATG	1 AAGATTCTGAAGAAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACTGAA 	4 AGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTCC	4 ACAAAAGACCGTTTGTGTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCCAT	1 TIGICGAGAGAGGGGTGTICICIGAGGACCGCACACGTTICIAIGGTGCAGAAAITGTC	1 TCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAGGTTGGAG 	AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAA 	GGGATCACAGATGCAGCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA	1 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC	1 ATGTATGAAATGATGTGTGGGAGGTTACCTTTCTACAACCAGGACCATGAGAACTTTTT	1 GAATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTCTTCAGATGCAAAATCA	1 TIGCTITCAGGGCTCTTGATAAAGGATCCAATAAACGCCTTGGTGGAGGACCAGATGAT	1 GCAAAAGAAATTATGAGACACAGTTTCTTCTGGAGTAAACTGGCAAGATGTATATGAT	
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Search completed: February 15, 2006, 05:23:05 Job time : 638 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM nucleic - nucleic search, using sw model

Pebruary 15, 2006, 05:12:42 ; Search time 3879 Seconds
(without alignments)
11796.279 Million cell updates/sec Run on:

US-10-601-311-2 978 1 tctacaacccatcataaaag.....atggtatggactgcatggac 978

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

41078325 segs, 23393541228 residues Searched:

82156650 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b\_est1::\*
9b\_est2::\*
9b\_est4::\*
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9b\_gss2::\* EST: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Re

Description	AL117525 Homo sapi	AY399351 Homo sapi	AY399353 Mus muscu	BU520318 AGENCOURT	CA430499 UI-H-FH1-	BU703964 UI-M-FO0-	CV557292 UI-M-HZ0-	BI917703 603183679	CA867933 ir83c04.y	CD675747 fs27d11.y	CN459710 UI-M-HB0-	CF741213 UI-M-GH0-	BU055259 UI-M-FO0-	BU790247 in52e10.x	CN526605 UI-M-HNO-	CR854381 DKFZp468P	CA943661 ir83c04.x	CF723245 UI-M-GV0-	CF532847 UI-M-GH0-	CB247756 UI-M-FIO-	CB520675 UI-M-GIO-	CK640105 UI-M-HNO-
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## ALIGNMENTS

	HSM801048 1584 bp mRNA linear HTC 16-APR-2005 Homo sapiens mRNA; cDNA DKF2p434N0250 (from clone DKFZp434N0250). AL117525 HELT GI:5912042	Hico sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;	<pre>1 (bases 1 to 1584) Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.</pre>	The German cDNA Consortium Direct Submission Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ, German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp634N0Z50) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi.bin/products/cl.cgi?CloneID=DKFZp634N0Z50 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.		<pre>/note="v-akt murine tnymoma viral oncogene nomolog 3" 11584</pre>
RESULT 1 LOCUS LOC	RESULT 1 HSM801048 LOCUS DEFINITION ACCESSION VERSION	KEIWOKUS SOURCE ORGANISM	REFERENCE AUTHORS	CONSRIM TITLE JOURNAL	COMMENT	FEATURES BOUTCE	gene

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1440 bp DNA linear GSS 15-DEC-2003
Homo sapiens AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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1 (bases 1 to 1440)

1 (bases 1 to 1440)

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriars, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, Resp. T. Shinsky, J.J.,
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                             1339 GCAAAAGAAATTATGAGACACAGTTTCTTCTGTGGAGTAAACTGGCAAGATGTATGAT
                                GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT
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Science 302 (5652), 1960-1963 (2003)
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99.8%; Pred. No. 4.1e-245;
ive 0; Mismatches 2; Indels 0;
gene="DKFZp434N0250"
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 Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                        Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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                                gene trios
Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                       1. .1394
/organism="Mus musculus"
/mol type="genomic DNA"
/db xref="taxon:10090"
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/gene="AKT3"
/locus_tag="HCM0195"
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Best Local S
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VIRTUAL TRANSCRIPT, partial sequence,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston
Bukaryota; Metazoa; Chordata; Craniata; Glires; Rodentia;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (baese 1 to 1394)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Mang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
                                                                 CAGACAAAAGACCGTTTGTGTTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC
                                                                                                                             CATTIGLE
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Mus musculus AKT3 gene, VIRT
genomic survey sequence.
AY399353
AY399353.1 GI:39755342
GSS.
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Oy 37 TTTGACTATTTGAAACTACTAGGTAAAGGCACTTTTGGAAAAGTTATTTGGTTCGAGAG 96	-	Qy         157 GATGAAGTGGCACACACTCTAAACTGAAAGCAGAGTATTAAAGAACACTGGACACTTT 216           Db         144 GATGAAGTGGCACACACTCTTACTGAAAGCAGAGTACTAAAGAACACCAGACATCCATTT 203	Oy 217 TTAACATCCTTGAAATATTCCTTCCAGACAAAAGACCGTTTGTGTTTTGTGATGGAATAT 276	Oy         277 GITAATGGGGCCAĞCTGITITICCATITGTCGAGAGCGGGTGITCTCTGAGGACCGC 336           Db         264 GITAATGGCGAGAGACTGITITCCATITGTCGAGAGAGGGAGTGITCTCTGAGGACCGC 323	Oy 337 ACACGTTTCTATGGGAGAAATTGTCTCTGCCTTGGACTATCTACATTCGGAAAGATT 396		Qy         457 ACAGATTTTGGAATTTGGAAAGAGGATCACAGATGCAGCCACCATGAAGACATTCTGT 516	Qy         517 GGCACTCCAGAATATCTGGCACCAGAGGTAGAGATAATGACTGAGCAGCAGTA 576           Db         504 GGCACACCAGAGTACCTGGCACCAGAGGTATTAGAAGATAATGACTATGGCCGAGCCGTG 563	Oy 577 GACTGGTGGGCCTTGTCATGTATGAAATGATGTGTGGGAGGTTACCTTTCTAC 636	Oy 637 AACCAGGACCATGAGAACTTTTTGAATTAATAGAAGACATTAAATTTCCTCGA 696	Oy 697 ACACTCTTCAGATGCAAAATCATTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAA 756	GGCCTTGGTGGAGGACCAGATGATGCAAAAGAAATTATGAGACACAG-TTTCTTCTCTGG 	Oy 816 AGTAAACTGGGAAGATGTATATGATAAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAAC 875	Qy         976 ATCTGAGACAGATA-CTAGATATTTTGATGAGG-AATTTACAGCTCAGACTATTACAATA         933           Db         862 ATCTGAAACAGCCCGATATTTTGATGAAGAAATTTACAGCTCAGACTATTTACATA         921	Qy         934 ACACCACTGAAAATATGATGAGATGGTATGGACTGCATGGAC         978		.2479322
Oy 661 GAATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTCTTCAGATGCAAAATCA 720	Qy       721 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT 780         Db       1080 TTGCTTTCAGGGTCTTGATAAAGGATCCAAATAAACGNNNNNNNNNN	QY 781 GCAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840 Db 1140 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Qy 841 AAAAGCTIGTACCTCTTITAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT 900	Qy     901     GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT     960       Db     1260     GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAGTATGACGACGAC     1319	Qy 961 GGTATGGACTGCATGGAC 978 	BU520318 967 bp	ulus cDNA clone	S EST. Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus. REFERENCE 1 (bases 1 to 967)	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. David Rowe CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Plate: LiAM14099 row: 1 column: 05 High quality sequence start: 16 High quality sequence stop: 729. FEATURES Location/Qualifiers	<pre>BOUICE 1. :96 /</pre>	/clone="IMAGE:6518260" /tisque_type="undifferentiated limb" /lab host="DHIOB (phage-resistant)" /clone_lib="NHI MGC 134"	្លាំខក្ស	Query match Best Local Similarity 93.4%; Pred. No. 4.2e-200; Matches 883; Conservative 0; Mismatches 55; Indels 7; Gaps 6;

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov.

Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 AATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTCTTCAGATGCAAAATCAT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 TGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGATG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              782 CAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATA 841
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                          842 AAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTG
                                               GGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCAG
                                                                                                                                                                                                               542 AGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGGTTGTCA
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/clone="IMAGE:6406347"
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/tay stage="embryo 12.5dpc"
/lab_host="DH10B (TI phage resistant)"
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/strain="C57BL/6"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Umpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-racement: James Martin

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA

sequence: 1-42, AAT_rich#Low_complexity (matched compliment)

Seq primer: M13 FORWARD

POUXA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Momoo saptens"
//wol type="mRNN"
//db_xref="mRNN"
//db_xref="mRNN"
//db_xref="mRNN"
//db_xref="mRNN"
//db_xref="memble"
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//lab_host="mBHD8 (Life Technologies)"
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                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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0; Mismatches 5;
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TAG_SEQ=AGAATCCGGC"
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                                                                                                                                                                        Hominidae; Homo
                                               Homo sapiens
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               /notes="Organ: Brain; Vector: pYX- Asc; Site 1: EccR I; Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agazos gel. First strand cDNA was size fractionated on a 1% agazos gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, diseated with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGGCC. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of America Health (NIMH), Hemin Chin, Ph.D.,
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/clone_lib="NIH_BMAP_FOO"
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/organism="Mus musculus"

/mol type="mRNR"
/strain="c57BL/6"
/db_xref="taxon:10090"
/tissue_type="whole eye"
/tissue_type
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RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Conteat: Robert Strausberg, Ph.D.

Email: ggapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefil.html

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
CV557292 177 bp mRNA linear EST 22-OCT-2004 UI-M-HZ0-csv-g-14-0-UI.rl NIH_BMAP_HZ0 Mus musculus cDNA clone IMAGE:30689725 5', mRNA sequence.
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Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Richer Consortium/LLNL at:
http://image.llnl.gov
Richer Consortium/LLNL at:
Location/Qualifiers
                                                                                                                         ATGGTGCAGAAATTGTCTCTGCTTTGGACTATCTACATTCTGGAAAGATTGTGTGTACCGTG
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                    ATCTCAAGTTGGAGAATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTG
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1 (bases 1 to 703)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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BI917703 GI:16181501
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Hominidae; Homo.

1 (bases 1 to 641)
Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Wistow,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Human Lens cDNA (Normalized): fs"
/note="Organ: Bye; Vector: pCMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   f827d11.y1 Human Lens cDNA (Normalized): f8 Homo sapiens cDNA clone f827d11.y, mRNA sequence.
                                  249 AAAATTACAGATTTTGGACTTTGCAAAGAAGGGATCACAGATGCAGCCACCATGAAGACA 308
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   451 AAAATTACAGATTTTGGACTTTGCAAAGAAGGGATCACAGATGCAGCCACCATGAAGACA 510
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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Plate: 27 row: d column: 11
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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CD675747.1 GI:32177478
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Fax: 301 496 0078
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/note="Organ: Pancreas; Vector: pBluescript Size-selected on agarcse gel. Average insert size-1:
/note="Organ: Pancreas; Vector: pBluescript Size-1:
/n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue andocrine pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTTTTAACATCCTTGAAATATTCCTTCCAGACAAAAGACCGTTTGTGTTTTGTGATG 68
                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 656)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, T., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Milliams, T., Jackson, Y. and Bowers, Y. Cole, R., Tasgareishvili, R., Endocrine Panoreas Consortium

Upublished (2000)
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 486.
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similar to TR: Q9Y243 Q9Y243 PROTEIN KINASE B GAMMA.
                                                                                        CA867933.1 GI:27319482
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

Toba Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing Dy: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/mousefl.html

1 (bases 1 to 673)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Sciurognathi; Muroidea; Muridae; Murinae; Mus

This clone was contributed by the Brain Molecular Anatomy Project

1. .673 /organism="Mus musculus"

Location/Qualifiers

Seq primer: pYX-5

/db\_xref="taxon:10090" /clone="IMAGE:30649359"

/mol\_type="mRNA" /strain="C57BL/6"

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            using SPG RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (mg) was hybridized (COt 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center(NISC)."
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template for biotinylated RNA
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/tissue types:"Wholesey"
/dev stage="wholesey"
/dev stage="whole (Tiphage resistant)"
/lab_host="NutB BMAP HBO"
/clone lib="NIH BMAP HBO"
/clone lib="NIH BMAP HBO"
/clone lib="NIH BMAP HBO"
/site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel:First strand cDNA synthesis was primed with Oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nerrous System', supported by National Institute of Mental Health (NIMH)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGGAAAGTTATTTGGTTCGAGAGGGAAGTGGAAAATACTATGAAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 613.2; DB 7;
Pred. No. 2.9e-154;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                          62.7%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633;
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Best Local S:
Matches 633,
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EST 21-APR-2004

CMAS9710
UI-M-HBO-COV-e-16-0-UI.rl NIH BMAP\_HBO Mus musculus CDNA clone IMACE:30649359 5', mRNA sequence.

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

CN459710 CN459710.1 GI:46465436 EST.

Mus musculus Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,

ORGANISM

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BU055259 675 bp mRNA linear EST 26-AUG-2002
UI-M-FOO-bzp-j-23-0-UI.rl NIH BMAP_FOO Mus musculus cDNA clone
IMAGE:6405622 5', mRNA sequence.
Lower brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429
                                                                                                                                                                                                                                                                                                             61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAAGGCAAGTGGAAAATACTATGCT 120
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Mus musculus
Bukaryota, Metzooa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidea; Muridae; Mus.
1 (bases 1 to 675)
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                                                                                                                                                                                                                        190 GAAAGCAGAGTACTAAAAGAACACCAGACATCCATTTTAACATCCTTGAAATATTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 CATTTGTCGAGAGGGAGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT
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                                                                                                                                                                                                                                                                                                                                                    71 AAAGG-ACTITIGGGAAAGTTATTTTGGTTCGAGAGAGAGGCAAGTGGAAAATACTAIGCT
                                                                                                                                                                                                                                                                                                                                                                                               121 ATGAAGATTCTGAAGAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
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                                                                                                                                                                                      5
                                                                                                                                            691;
                                                                                                                                            Length
                                                                                                                                                                                    35; Indels
                                                                                                                                          Score 603.6; DB 6;
Pred. No. 1.1e-151;
0; Mismatches 35;
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BU055259.1 GI:22495349
                                                                                                                                        / Match 61.7%;
Local Similarity 94.6%;
hes 646; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="MudE:30618310"
/tismue_type="Muole brain"
/dev stage="Mtole brain"
/dev stage="1, 5, and 15 days newborn"
/deb_host="DH10B (T1 phage resistant)"
/clone="Ibx NIH BMAP_GH0"
/clone="Drigan: Brain"/ Vector: pYX- Asc; Site 1: EcoR I;
/clone 11b="NIH BMAP_GH0"
/note="Organ: Brain"/ Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer contenining a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF741213 691 bp mRNA linear EST 10-OCT-2003 UI-M-GHO-cli-c-19-0-UI.rl NIH BMAP_GHO Mus musculus cDNA clone IMAGE:30618210 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                            549
                                                                                                                                            609
                                                                                                                                                                                    547
                                                                                                                                                                                                                               699
                                                                                                                                                                                                                                                                    607
                                                                                                                                                                                                                                                                                                             729
                                                                                                   487
                                                                                                                                                                                                                                                                                                                                CTAATGGAAGACATTAAATTCCCCCGGAACACTCTCTCAGATGCAAAATCATTGCTTTCA 667
                 CTAGATAAGGATGGCCATATAAAATTACGGATTTTGGGCTTTGCAAAGAAGGGATCACA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. (bases 1 to 691)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health; Mammalian Gene Collection (MGC)
                                                        GAAGATAATGACTATGGCCGAGCCGTGGACTGGTGGGGCTTAGGTGTTGTCATGTATGAA
                                                                                                                                                                                                                                                     GAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGGTTGTCATGTATGAA
                                                                                                                                                                                                                               ATGATGTGGGAGGTTACCTTTCTACAACCAGGACCATGAGAAACTTTTTGAATTAATA
                                                                                                                                                                                                                                                                                                             670 TTAATGGAAGACATTAAATTTCCTCGAACACTCTTCAGATGCAAAATCATTGCTTTCA
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Mus musculus
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BU790247 594 bp mRNA linear EST 11-OCT-2002 in52e10.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6125683 3' similar to TR:Q9X243 Q9X243 PROTEIN KINASE B GAMMA. ;, mRNA
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 617-495-8557
Email: dmeltcn@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue
Nashington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -400P from Gibco
High quality sequence stop: 439.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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I (bases 1 to 594)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hallaer, L., Marran, M., Pape, D., Wylle, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Buldocrine Pancreas Consortium
Unpublished (2000)
                                                                                                                                                                                                                  GTCTCTGCTTTGGACTATCTACATTCTGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG
                                                                                                                         602 ATGTATGAAATGATGTGTGGGAAGGTTGCCTTTCTACAACCAGGATCATGAG-AACTCTTT
                                                                                     421 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAA
                                                                                                                                                                                                                                                                                                                                                              GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                              542 GAGGTATTAGAAGATAATGACTATGGCCGAGCCGTGGACTGGTGGGGGCTTANGTGTTGTC
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Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Homo sapiens"
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/dev stage="whole brain"
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Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer contening a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental "NIMH", Hemin Chin, Ph.D.,
NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLOM Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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94.8%; Pred. No. 2.2e-150;
live 0; Mismatches 33;

    .675
    /organism="Mus musculus"
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clone="IMAGE:6405622"
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/dew stage="Jype="Opper near
/dew stage="Jype="Opper near
/lab_host="DH10B (T1 phage resistant)"
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/note="Organ: Head; Vector: pXx-Asc; Site l: EcoR I;
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Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
                   DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pXx-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACACGTTTCTATGGTGCAGAAATTGTCTCTGCCTTGGACTATCTACATTCCGGAAAGAT 395
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    CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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Pred. No. 5.1e-149;
0; Mismatches 48;
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                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="CS7BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30650717"
/tissue_type="Upper Head"
                                                                                                                                                                                      1. .710
/organism="Mus musculus"
                                                                                                                                                              Location/Qualifiers
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Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MD 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
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Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                 60.7%; Score 594; DB 5; Length 594;
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AUTHORS
TITLE
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        814 GGAGTAAACTGGCAAGATGTATATGATAAAAAGCTTGTACCTCTTTTAAACCTCAAGTA 873

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        541 GGAGTAAACTGGCAAGATGTAACAAAAGCTTGTACCTCCTTTTAAGCCTCAAGTA 600

        Qy
        874 ACATCTGAATACTAGATATTTAGA TGAAGAATTTACAGCTCAGACTATTACAAGT
        932

        Db
        601 ACATCTGAACAGCCCCGATTTTTGATTGATTAAAGATTTACAGCTCAGACTATTACAAT
        600

        Qy
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        Db
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        600

        Qy
        933 AACACCACCTGAAAAATTTAGATGATTTAGATGACTGCATGGAC
        978

        Db
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        978
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Search completed: February 15, 2006, 06:28:03 Job time : 3884 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

- nucleic search, using sw model OM nucleic

Run on:

Title: Perfect score:

US-10-601-311-2 978 1 tctacaacccatcataaaag.....atggtatggactgcatggac 978 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

5883141 segs, 28421725653 residues

Searched:

11766282 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database

gb\_ba:\*
gb\_onv.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	D	Description
	978	100.0	1436	9	BD251227	BD251227 Human Akt
8	978	100.0	1436	9	AX026530	AX026530 Sequence
e	978	100.0	1440	9	BD142211	BD142211 Method fo
4	978	100.0	1440	11	AY335691	AY335691 Synthetic
Ŋ	978	100.0	1440	11	AY893474	AY893474 Synthetic
9	978	100.0	1440	11	AY893919	AY893919 Synthetic
7	978	100.0	1445	80	BC020479	BC020479 Homo sapi
80	978	100.0	1547	9	BD251226	BD251226 Human Akt
σ	978	100.0	1547	9	AR593589	AR593589 Sequence
10	978	100.0	1547	ø	AX026529	AX026529 Sequence
11	978	100.0	1547	۵	HSA245709	AJ245709 Homo sapi
12	978	100.0	1651	9	CQ714620	CQ714620 Sequence
13	978	100.0	1706	8	AF085234	AF085234 Homo sapi
14	978	100.0	1708	œ	AF124141	AF124141 Homo sapi
15	978	100.0	2367	9	BD260777	BD260777 Human pro
16	978	100.0	2811	8	AF135794	AF135794 Homo sapi
17	949.8	97.1	1570	9	BD250154	BD250154 AKT nucle
18	949.8	97.1	1570	9	AR651346	AR651346 Sequence

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## ALIGNMENTS

BD251227  Human Akt-3.  BD251227  BD551227  GG:33060997  BP 2002535964-A/2.  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (craniata; Vertebrata; Buteleostomi; human)  BUSATYOLa; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; human)  BUSATYOLa; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; humannalia; Butheria; Buarchontoglires; Primates; Catarrhini;	Incommission to 1436) Masure, S.L.J. and Richardson, A. Human Akt-3 Patent: JP 2002535964-A 2 29-OCT-2002;	OS Homo sapiens (human) PN JP 2002555964-A/2 PD 29-OCT-2009 PF 17-DEC-1999 JP 2000589669 PR 22-DEC-1998 GB 9828375.7 PI STEFAN LEO JOZEF MASURE, ALAN RICHARDSON	SLN15/09, AG1K31/713, i SLP35/00, AG1P43/00, CO7K16, 12, CL2Q1/02, CL2Q1/48, GQ1N33/; CL2N15/00, CL2N15/00, Human Akt-3	FH Key Location/Qualifiers FT source 11435 FT Location/Qualifiers 11436 /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"
RESULT 1 BU251227 LOCUS B DEFINITION H ACCESSION B KEYWORDS SOURCE ORGANISM H M	REFERENCE 1 AUTHORS M TITLE H JOURNAL P	COMMENT	a O	F F FEATURES SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels
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                             DNA
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                          AX026530 1436 bp
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Matches 978; Conservative 0; Mismatches 0;
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AY335691 SYN 08-JUN-2005 Synthetic construct Homo Bapiens v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, partial cds.

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                  ATGAAGATTCTGAAGAAGAAGTCATTATTGCAAAGGATGAAGTGGCACACACTCTAACT
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PP 22-AUG-2001 WO 2001JP007179
PP 22-AUG-2001 WO 2001JP007179
PP 22-AUG-2000 UP 00P 251529
PP 22-AUG-2000 UP 00P 251529
PP AGINSS/17, AGINSS/45, AGINSS/39, 395, AGINK45/00, AGIP43/00, AGIP3/00, PC AGIPAS/17, AGINSS/17, AGINSS/18, AGINSS/18, AGINSS/18, AGINSS/18, AGINSS/10, PC AGIPAS/10, COTKIA/47, COTKIA/18, CI2NI/15, CI2NI/19 PC C12P21/02, CI2NI/15/09, GOINSS/50, GOINSS/50, GOINSS/68, AGINSS/68, AGINSS/68,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1440)

1 struct., Fujita,N. and Sato,S.

Method for controlling apoptosis and polypeptide controlling
Patent: WO 0215925-A 5 28-FEB-2002;

KYOWA HAKKO KOGYO CO LTD,TAKASHI TSURUO,NAOYA FUJITA,SAORI SATO
OS Homo sapiens (human)
PN WO 0215925-A/5
                                                                                                       TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT
                                                                                                                                                                                       GCAAAAGAAATTATGAGACACAGTTTCTTCTTCTGGAGTAAACTGGCAAGATGTATATGAT
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                                                                                TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT
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Location/Qualifiers
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BD142211.1 GI:23237156
WO 0215925-A/5.
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AY893474 linear SYN 16-MAR-2005 Synthetic construct Homo sapiens clone FLH127839.01X v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, complete cds.

AY893474.1 GI:60819745
Human ORR Project.
Synthetic construct
synthetic construct
the sequences, artificial sequences.

Other sequences, artificial sequences.
Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
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CATTIGICAGAGAGAGCGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 765
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                                                                                                                                                     GTCTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
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                                                             GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
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LiaBaer, J. and Brizuela, L.

Direct Submission

Submitted (02-UUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2003, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TW) cloning system between the Sall and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
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KVILVREKAGGKYYAMKILKKEVIIAKDEVAHTUTESRSVLKAWTHPFITSLKGYSPQTK
DRLCFVMFYNNGGELFFILERERVESEDRTRFYGAETVSALDYLHSGKIVYRDLKLEN
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VMYEMMCGRLPFRANCHELIAMEDIKFPRTLSSDAKSLLSGLIKODWWGLGV
PDDAKEINRHSFFSGVNWODYDKKLVPPFREQVTSETDTRYFDEEFTAQTITITPPE
KYDEDGMDCMDNERRPHFPQFSYSASGREL"
                                                 other sequences; artificial sequences.

(bases 1 to 1440)

(hark, J. Hu,Y., Mutthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A., Hutti,J.E., Cantley,L.C., LaBaer,J., Harlow,E. and Brizuela,L. Building a human kinase gene repository: Bioinformatics, molecular Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
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/clone_lb="First strand cDNA_from_placenta and brain"
/lab_hoste:"bHSalpha_T1_resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAAATACTATGCT
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|gene="AKT3"
|note="protein kinase B, gamma; Mutations: Stop->Leu"
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|mol_type="mkNA"
|db_xref="taxon:32630"
|clone="FLH000146.01L"
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Synthetic construct Homo sapiens clone FLH127915.01L v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, partial cds. AX893919 GI:60831074
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synthetic construct
synthetic construct
other sequences; artificial sequences.

1 (bases 1 to 1440)
Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Kounding, M., Hu, Y., Zuo, D. and LaBaer, J.

Cloning of human full-length CDS FLEXGene in
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Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
Direct Submission
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    766 GICTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 ATGTATGAAATGATGTGGGGGGGTTACCTTTCTACAACCAGGACCATGAGAAACTTTTT
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                                                                                               GTCTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG
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S Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.

Direct Submission

Direct Submission

Submitted (04-JAN-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA a collection of human full-length

This CDS clone is a part of a collection of human full-length

expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned with normalized stop-codon. AttB

recombination sites have been added to either end of the ORF and
directionally cloned using the Gateway cloning system into pDONR

201. Additional sequences in the clone: 'ACC' before the 'ATG'

(corresponding to ribosomal binding site and Kozak consensus
sequence-verified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="FLH127839.01X"
/lab host="Escherichia coli DH5alpha Tl resistant"
/lab host="Escherichia coli DH5alpha Tl resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MSDVTIVKEGWVQKRGEVIKNWRPRYFLLKTDGSFIGYKEKPQD
VDLPYPLNNPSVAKCQLMKTERPKPNTFIIRCLQWTTVIERTFHVDTPEEREEWTEAI
QAVADRLQRQEEERMNCSPTSQIDNIGEEEMDASTTHHKRKTWNDFDYLKLLGKGTFG
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DRLCPWEYVNGGELFFHLSRERVFSEDRTRFYGAELVSALDDYLHSGKIVYRDLKLEN
LMLDGHIKITDFGLGTIDAATWKTFCGTPEYLAPEVLEDNDYGRAVDWMGLGV
VMYEMMCGHIKITDFGLFGTIDAATWKTFCGTPFXLASDAKSLLGGLIKOPRKRLGG
PDDAKEIMRHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEEFTAQTITITPPE
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/transl_table=11
/product="v-akt murine thymoma viral oncogene-like 3"
/protein_id="MAX36511.1"
/db_xref="G1:60819746"
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Cloning of human full-length CDS FLEXGene in Gateway (TM) recombinational vector system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
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/gene="AKT3"
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Db   826 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAAGAA   885	000   000	BESULT 7 BECO20479 BCC2050 BCC2050 BCC2050 BCC2050 BCC2050 BCC2050 BCCCESSION BCC20479 BCCCESSION BCC20479 ACCESSION BCC20479.1 GI:18042842 KEWWORDS Homo sapiens (human) OCGANISM BCC20479.1 GI:18042842 BCCCCESSION BCC20479.1 GI:18042842 BCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
COMMENT  This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.  This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone:  'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.  FEATURES  1. 1440    Organism="Synthetic construct"   Account of the Consensus Synthetic construct"   Account of the Corpus of Synthetic construct   Account of Synthetic Construct   Account of Corpus of Synthetic Construct   Account of Synthetic Construct of Synthetic Construct   Account of Synthetic Construct of	/ (db. x=rye="mixtor") / (db. x=rye="mixtor") / (db. x=rye="mixtor") / (db. x=ref="mixtor")	Duery Match   100.0%;   Score 978;   DB 11;   Length 1440;   Best Local Similarity   100.0%;   Pred. No. 4.1e-206;   Matches 978;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;   Indels   0

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1112 GAATTAATTAATGGAAGACATTAAAATTTCCTCGAACACTCTCTTCAGATGAAAATCA 1171
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JP 2002535964-A/1.
Homo sapiens (human)
Homo sapiens (buracoa; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT
                                        GAAAGCAGAGTATTAAAGAACACTGAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC
                                                                                                                                                                                                                                                                        CATTIGLICAGAGAGGGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT
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/product="ART3" protein"
/product="ART3" protein"
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KV11LVREKASGKYYAMKILKKEVIIANDEWHTLYTESRVLKWTRHPFLTSLLGKGTFG
KV11LVREKASGKYYAMKILKKEVIIASBRTRFYGAEIVSALDYLHSGKIVYRDLKLEN
DRLCFVMFYNNGGELFFHLARRENVESBRTRFYGAEIVSALDYLHSGKIVYRDLKLEN
DRLCFVMFYNNGGELFFHLARRENVESBRTRFYGAEIVSALDYLHSGKIVYRDLKLEN
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DRLCFVMFYNNGGELFFHLANDIKKLPFELILMEDIKFPRTLSSDAKSLLSGLLIKOPNKALGGG
PDDAKEINMHSFFSGVNWQDVYDKKLVPPFKPQVTSETDTRYFDEEFTAGTITITPPE
KYDEDGMDCMDNERRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: h Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 32307164.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                         Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: egapbs.r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="synonyms: PKBG, PRKBG, DKFZP434N0250, RAC-gamma,
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human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Lissue Lype="Eye xetinoblastoma"
Cline Lib="WIH MGC_67"
/lab_host="DHIOB"
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Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAC-PK-gamma, STK-2"
/db_xref="GeneID:10000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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'gene="AKT3"
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GCAAAAAGAAATTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATGATT 1255
956 GAGGTGTTAGAAGATAATGACTATGCCCGAGCAGTAGACTGGTGGGGGCCTAGGGGTTGTC 1015
                                                                                                                  TIGCTITCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT 1195
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al Similarity 100.0%; Pred. No. 4.1e-206;
978; Conservative 0; Mismatches 0;
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Chiron Corporation, Emeryville, CA
Location/Qualifiers
1. .1547
/organism="unknown"
/mol_type="genomic DNA"
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PC C12Q1/48, G01N33/15, G01N33/50, G01N33/53, G01N33/566//C12P21/08,
PC C12N15/00, A61K37/60
CC Human Akt-3
Location/Qualifiers
FT source
1. 1547
FT
                                                                                           DS Homo sapiens (human)
PN JP 2002535964-A/1
PD 29-OCT-2002
PF 17-DEC-1999 GB 9828375.7
PI STEFAN LEO JOZEF MASURE, ALAN RICHARDSON
PC C12N15/09, A61K31/713, A61K38/53, A61K39/395, A61K48/00, PC
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Location/Qualifiers
                                           Human Akt-3
Patent: JP 2002535964-A 1 29-OCT-2002;
JANSEN PHARMACEUTICA NV
OS Homo sapiens (human)
PN JP 2002535964-A/1
PD 29-OCT-2002
PF 17-DEC-1999 JP 2000589669
PR 22-DEC-1999 GB 9828375.7
PI STEFAN LEO JOZEF MASURE, ALAN RICHARDSON
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Masure, S.L.J. and Richardson, A.
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/mol_type="unassigned DNA"
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                                              CATTTGTCGAGAGCGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT
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                                 CATTIGICGAGAGGGGGGTGTTCTCTGAGGACCGCACACGTTTCTAIGGTGCAGAAATT
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             CAGACAAAAGACCGTTTGTGTTTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC
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MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN
PHARMACEUTICA NV (BE)
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AX026529
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1. .1547
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AX026529
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JOURNAL
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                                     CATTIGICGAGAGAGGGGGTGTICTCTGAGGACCGCACGTTTCTATGGTGCAGAATT
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                                                                                                                                                                  ATGAAGATTCTGAAGAAGAAGAAGCATTATTGCAAAGGATGAAGTGGCACACACTCTAACT
                                                                                                                                                                                                                 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAACATCCTTGAAATATTCCTTC
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                                                                                  AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGGAAGGCAAGTGGAAAATACTATGCT
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                                                                                      HSA245709 1547 bp mRNA linear PRI 15-APR-2005
Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).
AJ245709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / translation="MSDVTIVKEGWVQKRGEYIKWWRPRYFLLKTDGSFIGYKEKPQD
DVDPPLNNFSVAKCQLMKTERPKPWTFIIRCLGWTTVUERTFHVDVPEBREBWTBAI
QAVADELQRGEEBRWACSPTSOIDMIGEEBWDASTTHHKRYMNDFDYLKLGGGTFG
KVILVREKASGKYYAMKILKKEVIIAKDEVHTLTESRVLKWTRHPFLTSLKYSFQTK
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Submitted (25-AUG-1999) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation,
Turnhoutseweg 30, B-2340 Beerse, BELGIUM
Phosphorylation at Thr305 and at Ser472 necessary for activation.
Location/Qualifiers
1. 1547
//organism="Homo sapiens"
                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                 Mortier, E.,
                                                                                                                                                                                                                                                                          Masure,S., Haefner,B., Wesselink,J.J., Hoefnagel,E., Mortier,E., Verhasselt,P., Tuytelaars,A., Gordon,R. and Richardson,A. Molecular cloning, expression and characterization of the human serine/threonine kinase Akt-3
Eur. J. Blochem. 265 (1), 353-360 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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100.0%; Score 978; DB 8; Length 1547;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon start=1
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/db_xref="G1:5804866"
/db_xref="InterPro:IPR00719"
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/db_xref="InterPro:IPR00250"
/db_xref="InterPro:IPR00250"
/db_xref="InterPro:IPR01109"
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function="serine/threonine
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1. .>1547
/gene="Akt3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q43-44"
                                                                                                                                             AJ245709.1 GI:5804885
Akt-3; Akt3 gene.
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11. .1450
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VERSION
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FEATURES
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VDLPYPLNNESVAKCQLMKTBRPKDNTFIIRCLQWTTVIERTFHVDTPERREBWTEAI
ODADADALQROGEBERNMCSPTSQIDUIGEBENDASTTHHKKKTMNDFDYLKLLGKGTFG
KVILVREKASGKYYAMKILKKEVIIAKDBVAHTLTESRVLKNTRHPFLTSLKYSFGTK
DRLCFVMEYVNGGELPFHLSRERVFSEDRTRFYGAEIVSALDYLHSGKIVYRDLKLEN
VMYENMCGRLPFTGGLCKEGITDAATMKTFCCTPEYLAPEVLEDNDYGRAVDWMGLGV
VMYENMCGRLPFYNODHEKTFELILMEDIKPFRLSSDAKSLLSGLIKDPRKLGGG
PDDAKSIMRHSFPSOTWQDYVDKKLVPPFKRQVTSETDTRKPDEBFTAQTITITPPE
KYDEDGMDCMDNERRPHFPGFSYSASGRE"
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                                                                                                                                                                                                                                                                                       GATGAAGAATTTACAGCTCAGACTATTACAATAACACCCCCTGAAAAATATGATGAGGAT 1320
     1021 GAATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTCTTCAGATGCAAAATCA 1080
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                                                           1081 TIGCTTICAGGGCTCTIGATAAAGGATCCAAATAAACGCCTIGGTGGAGGAGGAGGATGAT
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                                                                                                                                                                                 AAAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT
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                                        TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan
University, Lab of Human Gene Research, No. 220, Handan Road,
Shanghai, People's Republic of China, 200433
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarhini,
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1 (bases 1 to 1706)

Li,X., Yu,L., Huang,H., Zhang,M., Zhao,Y. and Zhao,S.

Cloning of a novel human cDNA, STK-2, which encodes a serine-threonine protein kinase (STK) homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Homo sapiens STK-2 mRNA, complete cds.
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/db_xref="GI:17529663"
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/organism="Homo sapiens"
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tive 0; Mismatches 0;
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Patent: WO 02068579-A 554 06-SEP-2002;
PE Corporation (NY) (US)
Sequence 554 from Patent W002068579.
CQ714620
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Anomalidae; Homo.

Standard Homo.

Standard Homo.

Standard Homo.

Standard Homo.

A human protein kinase Bgamma with regulatory phosphorylation sites in the activation loop and in the C-terminal hydrophobic domain the activation loop and in the C-terminal hydrophobic domain to Biologozog.

AL D. Biol. Chem. 274 (14), 9133-9136 (1999)

CE 2 (bases 1 to 1708)

RS Brodbeck, D., Cron. P. and Hemmings, B.A.

Direct Submission.

AL Submitted (27-JAN-1999) Friedrich Miescher-Institut,

Maulbeerstrasse 66, Basel 4058, Switzerland

Location/Qualifiers
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/product="protein kinase."
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VMYSEWMCGRLPFYNQDHEKLFELILAMEDIKPPRTSSDAKSLLSGLLIKDDRKRLGGG
PDDAKEIMHHSFRSGVNWGDYDKKLVPPFKRQVTSETDTRYFDEEFTAQTITITPPE
KYDEDGMDCMDNERRPHFQFSYSASGRE"
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     GI:4757578
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Location/Qualifiers 1 . 2367
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xrefe="taxon:9606"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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GGGATCACAGATGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA
                                                                  1138 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT
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putative active phosphorylation site
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Patent: JP 2002539823-A 1 26-NOV-2002;
BIOVITHUM AB
OS Homo sapiens (human)
PN JP 2002539823-A/1
PD 26-NOV-2002
PF 23-MAR-1999 SE 9901115-7
PR X5-MAR-1999 SE 9901115-7
PI ANNELI ATTERSAND
PC C12N15/09,A01K67/027,C07K16/40,C12N1
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JP 2002539823-A/1.
Homo sapiens (human)
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Attersand, A.
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QY         901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAATATGATGAGGAT 960           Db         1315 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAATATGATGAGGAT 1374           QY         961 GGTATGGACTGCATGGAC 978           Db         1375 GGTATGGACTGCATGGAC 1392	Search completed: February 15, 2006, 09:13:51 Job time : 4973 secs GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	OM nucleic - nucleic search, using sw model Run on: February 15, 2006, 05:23:16 ; Search time 4968 Seconds (without alignments) 11190.196 Million cell updates/sec	US-10-601-311-2 score: 978 : 1 tctacaacccatcataaaagtable: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 5883141 Begs, 28421725653 residues Total number of hits satisfying chosen parameters: 11766282 Minimum DB seq length: 0 Maximum DB seq length: 2000000000  Post-processing: Minimum Match 00* Listing first 45 summaries	Database: GenEmbl:*  1: gb_ba:* 2: gb_in:* 3: gb_env:* 4: gb_om:* 5: gb_ov:* 6: gb_pat:* 7: gb_ph:* 8: gb_pr:* 9: gb_pr:*		Regult Query No. Score Match Length DB ID Description  1 978 100.0 1436 6 BD251227 BD251227 Human Akt 2 978 100.0 1440 11 AY33561 BD1251227 Human Akt 3 978 100.0 1440 11 AY33561 AY335691 Synthetic 6 978 100.0 1440 11 AY335919 Synthetic

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1306 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT 1365
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MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE)
PHARMACEUTICA NV (BE)
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ive 0; Mismatches 0; Indels
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    1436
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Sequence 2 from Patent W00037613.
AX026530 GI:10187718
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/organism="Homo mapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	Query Match Best Local Similarity 100.0%; Score 978; DB 6; Length 1440; Best Local Similarity 100.0%; Pred. No. 4.1e-206; Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACTATTTGAAACTACTAGGT 60	Qy         61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAAAAGGCAAGTGGAAAAATACTATGCT 120           Db         466 AAAGGCACTTTTGGAAAAGTTATTTTGGTTCGAGAGAAAGGCAAAATACTATGCT 525	Qy 121 ATGAAGATTCTGAAGAAGAGGTTATTGCAAAGGATGAAGTGGCACACACTCTAACT 180 	OY 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTTAACATCCTTGAAATATTCCTTC 240	Qy         241 CAGACAAAAGACCGTTTGTGTTTTGTGATGGAATATGTGATATGGGGGCGAGCTGTTTTC 300	QY         301 CATITGTCGAGAGAGGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT         360           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 361 GTCTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420	QY 421 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTTGCAAAGAA 480 	QY         481 GGGATCACAGATGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA 540	Qy         541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGCAGTAGACTGGGGCCTAGGGGTTGTC         600           1	601 AIGTALGAAATGATGTGCGAGGTTACCTTTCTACAACCAGGACCATGAGAAACTTTTT 1	Oy 661 GAATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTCTTCAGATGCAAAATCA 720	Oy 721 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT 780	Oy 781 GCAAAAGAAATTATGAGACACAGTTTCTTCTTCTGGAGTAAACTGGCAAGATGTATATGAT 840	Oy 841 AAAAAGCTIGTACCTCCTTITAAACCTCAAGTAACATCTGAGACAGATACTAGATATTT 900	Oy 901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT 960 
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA 540	Oy         541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTTGTC         600           Db         946 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGCTTGTC         1005	Oy 601 ATGTATGAAATGATGTGGGAGGTTACCTTTCTACAAGACCATGAGAACTTTTT 660	OY 661 GAATTAATATTAATGGAAGACATTAAATTTCCTCGAACACTCTCTTCAGATGCAAAATCA 720	Qy       721 TIGCTITCAGGGCTCTTGAIAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT 780         Db       1126 TIGCTITCAGGGCTCTTGAIAAAGGATCCAAATAAACGCCTTGGTGGAGGACCAGATGAT 1185	Oy 781 GCAAAAGAAATTATGAGACACAGTTTCTTCTGGAGTAAACTGGCAAGATGTATATGAT 840	Qy 841 AAAAAGCTTGTTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT 900	Qy 901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGATGAGGAT 960 	Qy         961 GGTATGGACTGCATGGAC         978           Db         1366 GGTATGGACTGCATGGAC         1383	RESULT 3 BD14221 FOREST 1000 PD14221	Method for controlling apoptosis and polypeptide controlling apoptosis.  Apoptosis.  BD142211	VENSION BU14Z11.1 G1:Z3Z3/125 KEYWORDS WO 02159Z5-A/S. SOURCE Homo sapiens (human) ORGANISM Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1440)	2 A	COMMENT OS Home sapiens (human) PN WO 0215925-A/5 PD 28-FEB-2002 PF 22-AUG-2001 WO 2001JP007179	PR 22-ANG-2000 JP 00P 251529 PI TAKASHI TSUNUO,NAOYA FUJITA,SAORI SATO PC AGIK38/17,AGIK38/45,AGIK39/395,AGIK45/00,AGIP43/00,AGIP3/08, PC AGIP35/00,	PC A61P43/00, CO7K7/04, CO7K14/47, CO7K16/18, C12N1/15, C12N1/19 PC , C12N1/21, C12N5/10, C12N1/21, C12N5/10, C12P21/02, C12N15/10, C12P21/02, C12N15/10, C01N33/50, G01N33/15, G01N33/56, G01N33/68 CC human Akt3	FH Key Location/Qualifiers FT Source 1. 1440 FT / Organism='Homo sapiens (human)'. FEATURES Location/Qualifiers Source 1. 1440

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                                         TCTACAACCCATCATAAAAGAAAGACAATGAATGAATTTTGACTATTTGAAACTACTAGGT
                                                             406 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACTATTTGAAACTACTAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (O.-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Bach CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD in-Tusion(TM) cloning system between the Sall and HindIII sites but the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="v-akt murine thymoma viral oncogene-like 3"
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DRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAEIVSALDYLHSGKIVYRDLKLEN
LMLDKOGHIRTATDFGLCKEGITDAATWKTFCCTPEYLAPEVLEDNDYGRAVDWWGLGY
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PDDAKSIMRHSFFSGWWQDVYDKKLVPPFKPQVTSETDTRYFDEEFTAQTITITPPP
KYDEDGMDCMDNERRPHFPQFSYSASGREL"
                                                                                                                                   A linear SYN 08-JUN-2005
murine thymoma viral
                                                                                                                                                                                                                                                                                                                              Park, J., Hu, Y., Murthy, T.V.S., Vannberg, F., Shen, B., Rolfs, A., Hutti, J.E., Cantley, L.C., LaBaer, J., Harlow, E. and Brizuela, L. Building a human kinase gene repository: Bioinformatics, molecular cloning, and functional validation

Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
15928075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="placenta and brain"
/clone lib="First strand cDNA from placenta and brain"
/lab_host="DH5alpha Il resistant"
/note="Vector: pDNR-Dual"
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Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,B.,
LaBaer,J. and Brizuela,L.
Direct Submission
                                                                                                                                   AY335691 1440 bp mRNA Synthetic construct Homo sapiens v-akt mu oncogene-like 3 (AKT3) mRNA, partial cds.
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other sequences; artificial sequences.
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/db_xref="taxon:32630"
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/trans1_table=11
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RESULT 5 AY893474

Score 978; DB 11; Length 1440; Pred. No. 4.1e-206;

100.0%; 100.0%;

Query Match Best Local Similarity

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AY893919 1440 bp mRNA linear SYN 16-MAR-2005 Synthetic construct Homo sapiens clone FLH127915.01L v-akt murine AY893919 16:00821014 AY893919 AY893919 16:00831074 Human ORF Project. synthetic construct synthetic construct synthetic construct linear sequences; attlificial sequences.
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                                       ATGAAGATTCTGAAGAAGAAGTCATTATTGCAAAGGATGAAGGTGGCACACACTCTAACT
                                                                                                                                                GAAAGCAGAGTATTAAAGAACACTCTACCCTTTTTAACATCCTTGAAATATTCCTTC
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                                                                                                                 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAACATCCTTGAAATATTCCTTC
                                                                                                                                                                                                                             CAGACAAAAGACCGTTTGTGTTTTTGTGATGGAATATGTTAATGGGGGGCGAGCTGTTTTTC
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/codon start=1
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/product="v-akt murine thymoma viral oncogene-like 3"
/protein id="AAX3611.1"
/protein id="AAX3611.1"
/protein id="AAX3611.1"
/bb.ref="mile:"AAX3611.1"
/db.ref="mile:"AAX3611.1"
/db.ref="mi
Synthetic construct Homo sapiens clone FLH127839.01X v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
from placenta and brain"
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This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pbONR 201. Additional sequences in the clone: "ACC" before the 'ATG'
                                                                                                                                                                                                                                                                             Shen, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J. Direct Submission
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                                                                                                      AY893474.1 GI:60819745

Human ORF Project.
synthetic construct
synthetic construct
other sequences, artificial sequences.

1 (bases 1 to 1440)
Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J.
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
Cloning of human full-length CDS FLEXGene in
Gateway (TM) recombinational vector system
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/mol_type="mkNA"
/db_xref="taxon:32630"
/clone="FLH127835.01%"
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BC020479 1445 bp mRNA linear PRI 28-JUL-2005 Homo sapiens v-akt murine thymcoma viral oncogene homolog 3 (protein kinase B, gamma), mRNA (cDNA clone IMAGE:3867931), partial cds.
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                           1006 ATGTATGAAATGATGTGGGGGGGGTTACCTTTCTACAACCCAGGACCATGAGAAACTTTTT 1065
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                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                        CATTIGLICAGAGAGAGGGGGGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT
                                                                                                                                                   GICTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG
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                                                                                                                                                                                                      Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA.

Cambridge, MA 02141, USA.

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.

This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library
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Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J. Cloning of human full-length CDS FLEXGene in Gateway (TM) recombinational vector system
                                                                                                                         2 (bases 1 to 1440)
Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and LaBaer, J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
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/lab_host="Escherichia coli
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1. .>1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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PDDAKEINRHSFSGSVNWQDYYDKKLVPPFKPQVTSETDTRYFDEEFTAQTITITPPE

KYDEDGMDCMDNERRPR
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergeran, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sancherz, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Dickson, M. C., Rodriguez, A. W., Touchman, J. W., Scheurz, J. Myers, R. M.,
Schnerch, A., Schein, J. E., Jones, S.J. and Marra, M. A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: h Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 32307164. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-WGC Project URL: http://mgc.nci.nih.gov
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/gene="AKT3"
/note="8ynonyms: PKBG, PKKBG, DKFZP434N0250, RAC-gamma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_67"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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GTCTCTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG
                                               GGGATCACAGATGCAGCCACCATGAAGACATTCTGTGGCACTCCAGAATATCTGGCACCA
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Reinhard,C. and Jefferson,A.B.
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Patent: US 6809194-A 1 26-OCT-2004;
Chiron Corporation; Emeryville, CA
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C12Q1/48,G01N33/15,G01N33/50,G01N33/53,G01N33/566//C12P21/08,
C12N15/00,
C12N5/00,AG1K37/60
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                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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17-DEC-1999 DP 2000589669
22-DEC-1998 GB 928375,7
STEFAN LEO JOZEF MASURE,ALAN RICHARDSON
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JANSER PHARMACEUTICA NV
OS Homo sapiens (human)
PN JP 2002535964-A/1
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 (bases 1 to 1547)
Masure,S.L.J. and Richardson,A.
Human Akt-ä
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JP 2002535964-A/1
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Bukaryota; Metazoa; Chordata; Cran: Mammalia; Butheria; Buarchontoglir: Hominidae; Homo.  AUTHORS Masure,S.L. and Richardson,A. TITLE Human akt. JOURNAL Patent: WO 0037613-A 1 29-JUN-2000 MASURE STEFAN LEO JOZEF (BE); RICHARMACENTICA NV (BE) FEATURES 1. 1547 AOZANIAR="Homo sapiens" / Ap_arref="taxon:9606"   Adb_xref="taxon:9606"	Query Match Best Local Similarity 100.0%; Pred. No. 4 Matches 978; Conservative 0; Mismatche: Oy 1 TCTACAACCCATCATAAAAGAAAGACAATGAA. Db 416 TCTACAACCCATCATAAAAAAAAAGAAATGAATGAA. Oy 61 AAAGGCACTTTTGGGAAAGTTATTTGGTTCGT	Db 476 AAAGGCACTTTTTGGGAAAGTTATTTTGGTTCG Qy 121 ATGAAGATTCTGAAGAAGAAGACTTTTTGC Db 536 ATGAAGATTCTGAAGAAAGAAGTCATTATTGC Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACTCC	Db 596 GAAAGCAGAGTATTAAAGAACACTAGACATCC Qy 241 CAGACAAAGACGCGTTGGTTTTGTGATGGAL Db 656 CAGACAAAAGACCGTTTGTGTTTTGTGATGGAL Qy 301 CATTTGTCGAGAGGGGGGTGTTCTGAGGAC Db 716 CATTTGTCGAGAAGGGGGGTGTTTCTGAGGAC	361 776 421 836	481 896 541 956	OY 601 ATGINICAMING TOTAGE SEASON OF THE COLT OF THE COLT OF STATES AND A STATES AN
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LMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDYGRAVDWMGLGY
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KYDEDGMDCMDNERRPHFPQFSYSASGRE"
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KVILVREKASGKYYAMKILKKEVIIAKDEVHTLTESRVLKOTTRHPFLTSLKYSFQTK
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Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).
AJ245709
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Eur. J. Blochem. 265 (1), 353-360 (1999)
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QY 901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATTGATGAGGAT 960	Ouery Match  Duery Match  Best Local Similarity 100.0%; Score 978; DB 6; Length 1651;  Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gape 0;  Although Matches 978; Conservative 0; Mismatches 0; Indels 0; Gape 0;  1 TCTACAACCCATCATAAAAAAAAAAAAAAAAAAAAAAA

07-MAY-1999

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Hominidae; Homo.

1 (bases) 1 to 1009)

Brodbeck, D., Cron, P. and Hemmings, B.A.
A human protein kinase Bgamma with regulatory phosphorylation sites in the activation loop and in the C-terminal hydrophobic domain 10092583
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   1353 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACCTGAAAAATATGATGAGGAT 1412
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PDDAKEINRHSFFSGVWWQUYVKKLVPPFKPQVTSETDTRYFDEEFTAQTITITPPE
KYDEDGMOCMINERRPHFPQPSYSASGRE"
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                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                       Homo sapiens protein kinase B gamma mRNA, complete cds.
AF124141
AF124141.1 GI:4757578
                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1708)
Brodbeck, D., Cron, P. and Hemmings, B.A.
Direct Submission
Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerstrasse 66, Basel 4058, Switzerland
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.7e-206;
Matches 978; Conservative 0; Mismatches 0;
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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CATTIGICAGAGAGCGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT
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